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OM protein - protein search, using sw model

Run on: December 10, 2003, 19:30:51 ; Search time 41 Seconds

(without alignments)
472.308 Million cell updates/sec

Title: US-09-897-645-1

Perfect score: 618

Sequence: 1 MRMIVGHGIDIEELASIESA.....ISHTDQFVTASVILENHES 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	618	100.0	122	19 AAW80612	S. pneumoniae prot
2	618	100.0	122	22 AAU37879	Streptococcus pneu
3	618	100.0	122	22 AAU38056	Streptococcus pneu
4	618	100.0	122	21 AAY88388	S-ydcB essential b
5	608	98.4	120	21 AAY58607	Streptococcus pneu
6	608	98.4	120	24 ABU02175	S. pneumoniae type
7	339	54.9	118	23 ABP27226	Streptococcus poly
8	328.5	53.2	119	21 AAY91289	Group B Streptococ
9	328.5	53.2	119	23 ABP27225	Streptococcus poly

10	302	48.9	119	23 ABB54157	Lactococcus lactis
11	301	48.7	117	22 AAU35183	Enterococcus faeca
12	251	40.6	121	21 AAY88389	B-ydcB essential b
13	251	40.6	121	22 AAM52130	Bacillus subtilis
14	243	39.3	120	23 AAU10694	B. subtilis ACPS u
15	233	37.7	118	23 ABB47581	Listeria monocytog
16	213	34.5	119	22 AAU33845	Staphylococcus aur
17	213	34.5	119	22 AAU36808	Staphylococcus aur
18	208	33.7	119	21 AAB14979	Staphylococcus aur
19	199.5	32.3	124	23 ABP39429	Staphylococcus epi
20	149.5	24.2	126	22 AAU38203	Salmonella typhi c
21	139.5	22.6	126	18 AAM16453	E. coli acyl carri
22	139.5	22.6	126	22 AAU34663	E. coli cellular p
23	136.5	22.1	126	22 AAU36126	Klebsiella pneumon
24	135.5	21.9	122	20 AAY34912	Amino acid sequenc
25	131.5	21.3	125	24 ABP80377	N. gonorrhoeae ami
26	128.5	20.8	138	22 AAU54107	Propionibacterium
27	126.5	20.5	135	20 AAY37110	Amino acid sequenc
28	122	19.7	1836	24 ABJ25404	Aspergillus fumiga
29	122	19.7	1857	24 ABJ26004	Helicobacter pylor
30	121.5	19.7	119	22 AAU35774	Yeast fatty acid s
31	111.5	18.0	1887	23 ABB08801	Yeast fatty acid s
32	111.5	18.0	1887	23 ABB08802	Yeast fatty acid s
33	111.5	18.0	1887	23 ABB08803	Yeast fatty acid s
34	111.5	18.0	1887	23 ABB08804	Yeast fatty acid s
35	111.5	18.0	1887	23 ABB08805	Yeast fatty acid s
36	111.5	18.0	1887	23 ABB08806	Yeast fatty acid s
37	111.5	18.0	1887	23 ABB08807	Yeast fatty acid s
38	110.5	17.9	135	22 AAG92481	C glutamicum prote
39	107.5	17.4	1884	23 ABP73852	Candida albicans e
40	99.5	16.1	131	22 AAB76585	Corynebacterium gl
41	96.5	15.6	166	23 ABP09066	Human ORFX protein
42	91.5	14.8	785	22 ABG10690	Novel human diagno
43	89	14.4	245	22 ABB52780	Escherichia coli p
44	85	13.8	309	22 AAB27223	Human EXMAD-1 SEQ
45	80.5	13.0	208	23 ABP38633	Staphylococcus epi

ALIGNMENTS

RESULT 1
ID AAW80612 standard; Protein; 122 AA.

XX AAW80612;

XX 24-DEC-1998 (first entry)

XX S. pneumoniae protein of unknown function.

XX Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;

XX virulence; antibody; infection; detection; treatment; hypothetical;

XX cell wall biosynthetic; external target; minimal gene set protein.

XX Streptococcus pneumoniae.

XX WO9826072-A1.

XX 18-JUN-1998.

XX 09-DEC-1997; 97WO-US22578.

XX 13-DEC-1996; 96US-0036281.

XX (ELIL) LILLY & CO ELI.

XX Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;

XX Mills BJ, Norris FH, Peery RB, Rocky PK, Rostock PR;

XX Skatrud PL, Smith MC, Solenberg PJ, Treadway PJ;

XX Young Bellido ML;

XX WPI; 1998-348529/30.

DR N-PSDB; AAV65294.
XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
PT for evaluating gene expression, and identification of virulence
PT genes

PS Claim 3; Page 177; 333pp; English.

CC This sequence represents a Streptococcus pneumoniae protein of unknown
CC function. The invention provides DNA sequences (AAV65201 to AAV65304)
CC from the Streptococcus pneumoniae genome and corresponding protein
CC sequences (AAV80605 to AAV80728). The protein sequences are classified as
CC hypothetical, cell wall biosynthetic, external target, or minimal gene
CC set proteins. A recombinant host containing a vector comprising any of
CC the above nucleic acids can be used for the recombinant expression of the
CC proteins. The invention also provides a DNA chip having arrayed on it at
CC least 15 base pair fragment of any one or more of these DNA sequences.
CC The DNA chip can be used for evaluating gene expression in S.
CC pneumoniae and for identifying virulence genes in S. pneumoniae.
CC Antibodies that selectively bind to the above proteins or peptide
CC fragments can be used to treat S. pneumoniae infection. The antibodies
CC can also be used to detect S. pneumoniae cells.

XX Sequence 122 AA;

Query Match 100.0%; Score 618; DB 19; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.7e-69;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRMIVGHGIDIEELASIESAVTRHEGFAKRVLTQAEMERFTSLKGRQIEYLAGRWSAKE 60
DB 1 MRMIVGHGIDIEELASIESAVTRHEGFAKRVLTQAEMERFTSLKGRQIEYLAGRWSAKE 60

OY 61 AFSKAMGTGISKLGFDLEVINNENRGAPYFSQAPPSGKIWLSTSHDQFVTASVILENH 120
DB 61 AFSKAMGTGISKLGFDLEVINNENRGAPYFSQAPPSGKIWLSTSHDQFVTASVILENH 120

OY 121 ES 122
DB 121 ES 122

RESULT 2
AAU37879
ID AAU37879 standard; Protein; 122 AA.

XX AAU37879;
AC
XX
DT 14-FEB-2002 (first entry)

XX Streptococcus pneumoniae cellular proliferation protein #308.

XX Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.

XX Streptococcus pneumoniae.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

XX 23-MAY-2000; 2000US-206848P.

XX 26-MAY-2000; 2000US-207272P.

XX 23-OCT-2000; 2000US-242578P.

XX 27-NOV-2000; 2000US-253625P.

XX 22-DEC-2000; 2000US-257931P.

XX 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
DR N-PSDB; AAS55738.

PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX Example 3; Seq ID No 13472; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 122 AA;

Query Match 100.0%; Score 618; DB 22; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.7e-69;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRMIVGHGIDIEELASIESAVTRHEGFAKRVLTQAEMERFTSLKGRQIEYLAGRWSAKE 60
DB 1 MRMIVGHGIDIEELASIESAVTRHEGFAKRVLTQAEMERFTSLKGRQIEYLAGRWSAKE 60

OY 61 AFSKAMGTGISKLGFDLEVINNENRGAPYFSQAPPSGKIWLSTSHDQFVTASVILENH 120
DB 61 AFSKAMGTGISKLGFDLEVINNENRGAPYFSQAPPSGKIWLSTSHDQFVTASVILENH 120

OY 121 ES 122
DB 121 ES 122

RESULT 3
AAU38056
ID AAU38056 standard; Protein; 122 AA.

XX AAU38056;

XX 14-FEB-2002 (first entry)

XX Streptococcus pneumoniae cellular proliferation protein #485.

XX Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.

XX Streptococcus pneumoniae.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

XX 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
XX
DR MPI; 2001-611495/70.
DR N-PSDB; AAS55915.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Example 3; Seq ID No 13649; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 122 AA;
XX
Query Match 100.0%; Score 618; DB 22; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.7e-69;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRMIVGHGIDIEELASIESAVTRHEGFAPKRVLTAEQEMERFTSLKGRQIEYLAGRWSAKE 60
Db 1 MRMIVGHGIDIEELASIESAVTRHEGFAPKRVLTAEQEMERFTSLKGRQIEYLAGRWSAKE 60
QY 61 AFSKAMGTGISKLGFDQLEVLNNRERGAPYFSQAPFSGKIWLISHTDQFTVTAIVLEENH 120
Db 61 AFSKAMGTGISKLGFDQLEVLNNRERGAPYFSQAPFSGKIWLISHTDQFTVTAIVLEENH 120
QY 121 ES 122
Db 121 ES 122
XX
RESULT 4
ID AAY88388 standard; Protein; 156 AA.
XX
AC AAY88388;
XX
DT 25-JUL-2000 (first entry)
XX
DE S-ydCB essential bacterial protein amino acid sequence.
XX
KM Bacteria; S-ydCB; Streptococcus pneumoniae; antibacterial compound;
KM acyl carrier protein synthase; identify; bacterial infection; treatment.
XX
OS Streptococcus pneumoniae.
XX

PN WO200018952-A1.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US22666.
XX
PR 30-SEP-1998; 98US-0163446.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Fritz C, Youngman P, Guzman L;
XX
DR MPI; 2000-303457/26.
DR N-PSDB; AAA13270.
XX
PT Identifying new antibacterial agents particularly against Streptococcus
PT pneumoniae, uses S-ydCB polypeptide from S. pneumoniae and B-ydCB
PT polypeptide from Bacillus subtilis -
XX
PS Claim 17; Fig 1; 58pp; English.
XX
CC This sequence represents the protein encoded by the essential bacterial
CC gene S-ydCB from Streptococcus pneumoniae. B-ydCB is an S-ydCB ortholog
CC from Bacillus subtilis. The gene encodes a protein which has structural
CC characteristics of acyl carrier protein synthase and displays synthase
CC activity in vitro. The protein is used in a method for identifying an
CC antibacterial agent, which comprises contacting an S-ydCB or B-ydCB
CC polypeptide with a test compound and detecting an interaction between the
CC polypeptide and the test compound, where the interaction indicates that
CC the compound is an antibacterial compound. Antibacterial agents
CC identified using the method may be used to treat a bacterial infection,
CC especially Streptococcus pneumoniae in mammals, especially a human or
CC rodent. The method can be configured for high throughput screening of
CC numerous candidate antibacterial agents, and identified agents should
CC have a broad spectrum of antibacterial activity.
XX
SQ Sequence 156 AA;
XX
Query Match 100.0%; Score 618; DB 21; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.8e-69;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRMIVGHGIDIEELASIESAVTRHEGFAPKRVLTAEQEMERFTSLKGRQIEYLAGRWSAKE 60
Db 35 MRMIVGHGIDIEELASIESAVTRHEGFAPKRVLTAEQEMERFTSLKGRQIEYLAGRWSAKE 94
QY 61 AFSKAMGTGISKLGFDQLEVLNNRERGAPYFSQAPFSGKIWLISHTDQFTVTAIVLEENH 120
Db 95 AFSKAMGTGISKLGFDQLEVLNNRERGAPYFSQAPFSGKIWLISHTDQFTVTAIVLEENH 154
QY 121 ES 122
Db 155 ES 156
XX
RESULT 5
ID AAY58607 standard; Protein; 120 AA.
XX
AC AAY58607;
XX
DT 11-APR-2000 (first entry)
XX
DE Streptococcus pneumoniae acyl carrier protein synthase acps.
XX
KM Acyl carrier protein synthase; acps; infection; therapy;
KM diagnosis; antibacterial; antibiotic; Helicobacter pylori.
XX
OS Streptococcus pneumoniae.
XX
PN WO961452-A2.
XX
PD 02-DEC-1999.
XX

XX 27-MAY-1999; 99WO-US11704.
PF
XX
XX 28-MAY-1998; 98US-0087079.
PR
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA
XX
XX Pearson SC, Kallender H;
PI
XX
XX WPI; 2000-147027/13.
DR
XX N-PSDB; AAZ35350.
DR
XX
XX New isolated Streptococcus pneumoniae acps polypeptides, used to
PT develop products for treating, e.g. otitis media -
PT
XX
XX Claim 1; Page 31-32; 34pp; English.
PS
XX
XX The present sequence represents the acps protein of
CC Streptococcus pneumoniae strain 0100993 (NCIMB 40794), which is
CC phylogenetically related to proteins of the acyl carrier protein
CC synthase family. The invention provides acps polypeptides having
CC having at least 70% identity with the present sequence, as well as
CC acps polynucleotides, recombinant materials and methods for their
CC production. The polypeptides and polynucleotides can be used for
CC the diagnosis, prognosis or treatment of a disease related to the
CC expression or activity of acps. They can be used to treat microbial
CC diseases such as bacterial infections, particularly S. pneumoniae
CC infections, to prevent infections and to identify agonists and
CC antagonists useful as antibacterial compounds. They can also be
CC used to prevent bacterial adhesion to mammalian, extracellular
CC matrix proteins on in-dwelling devices or to extracellular matrix
CC proteins in wounds, to block bacterial adhesion between mammalian,
CC extracellular matrix proteins and bacterial acps proteins that
CC mediate tissue damage and/or to block the normal progression of
CC pathogenesis in infections other than by the implantation of
CC in-dwelling devices or by other surgical techniques. The
CC antibacterial compounds can be used in the treatment of
CC Helicobacter pylori (Hp) infections, to decrease the advent of
CC Hp-induced cancers, such as gastrointestinal carcinoma, and also to
CC prevent, inhibit and/or cure gastric ulcers and gastritis. They
CC can also be used for treating e.g. otitis media, conjunctivitis,
CC pneumonia, bacteraemia, meningitis, sinusitis, pleural empyema and
CC endocarditis.
CC
XX
SQ Sequence 120 AA;
Query Match 98.4%; Score 608; DB 21; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.7e-68;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAEEMERFTSLKGRQIEYLAGRWSAKEAF 62
Db 1 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAEEMERFTSLKGRQIEYLAGRWSAKEAF 60
QY 63 SKAMGTGISKLGFDLEVLNNERGAPYFSQAPFSGKIWLSTHTDQFVTASVILEENHES 122
Db 61 SKAMGTGISKLGFDLEVLNNERGAPYFSQAPFSGKIWLSTHTDQFVTASVILEENHES 120
RESULT 6
ABU02175
ID ABU02175 standard; Protein; 120 AA.
XX
XX AC ABU02175;
XX DT 11-FEB-2003 (first entry)
XX
XX S. pneumoniae type 4 strain protein from coding region #1752.
XX
XX Bacterial meningitis; pneumonia; sepsis; otitis media;
KW ear infection; antiinflammatory; antibacterial; immunostimulant;
KW auditory; respiratory; gene therapy; vaccine.
XX

OS Streptococcus pneumoniae type 4 strain.
XX
XX PN WO200277021-A2.
XX
XX PD 03-OCT-2002.
XX
XX PF 27-MAR-2002; 2002WO-IB02163.
XX
XX PR 27-MAR-2001; 2001GB-0007658.
XX
XX PA (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX
XX PI Masignani V, Tettelin H, Fraser C;
XX
XX DR WPI; 2003-040579/03.
DR N-PSDB; ABX07464.
XX
XX
XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
PT or ear infection -
XX
XX
XX Claim 1; SEQ ID No 3504; 56pp; English.
PS
XX
XX The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
CC ABS56454. Also included are an antibody which binds one of the
CC proteins, treating a patient by administering the protein, DNA or
CC antibody (in a composition), a kit comprising first and second primers,
CC which are the nucleic acid cited above or fragments between nucleotides
CC 8-100 of a sequence not defined in the specification, for amplifying a
CC target sequence contained within a Streptococcus nucleic acid sequence,
CC where the first primer is substantially complementary to the target
CC sequence and the second primer is substantially complementary to the
CC complement of the target sequence, and where the parts of the primers
CC having substantial complementarity define the termini of the target
CC sequence to be amplified, assay comprising contacting a test compound
CC with the protein, and determining whether the test compound binds to the
CC protein and a Streptococcus pneumoniae bacterium, where one or more
CC genes encoding the proteins has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present coding sequence is one of
CC the 2469 proteins expressed by the identified coding regions from the
CC genomic sequence.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 120 AA;
Query Match 98.4%; Score 608; DB 24; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.7e-68;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAEEMERFTSLKGRQIEYLAGRWSAKEAF 62
Db 1 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAEEMERFTSLKGRQIEYLAGRWSAKEAF 60
QY 63 SKAMGTGISKLGFDLEVLNNERGAPYFSQAPFSGKIWLSTHTDQFVTASVILEENHES 122
Db 61 SKAMGTGISKLGFDLEVLNNERGAPYFSQAPFSGKIWLSTHTDQFVTASVILEENHES 120
RESULT 7

ABP27226
ID ABP27226 standard; Protein; 118 AA.
XX AC ABP27226;
XX DT 02-JUL-2002 (first entry)
XX DE Streptococcus polypeptide SEQ ID NO 3628.
XX KM Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
OS Streptococcus pyogenes.
PN WO200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001; 2001WO-GB04789.
XX PR 27-OCT-2000; 2000GB-0026333.
PR 24-NOV-2000; 2000GB-0028727.
PR 07-MAR-2001; 2001GB-0005640.
XX PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tetelin H;
XX WPI; 2002-352536/38.
DR N-PSDB; ABN67857.
PT New Streptococcus protein for the treatment or prevention of infection
or disease caused by Streptococcus bacteria, such as meningitis, and
for detecting a compound that binds to the protein -
PS Claim 1; Page 3517; 4525pp; English.

The invention relates to a protein (ABP25413-ABP30895) from group B
streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
the specification. The proteins have antibacterial and antiinflammatory
activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and
antibodies that bind (I) are used in the manufacture of medicaments for
the treatment or prevention of infection or disease caused by
Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
Nucleic acids encoding (I) are used to detect Streptococcus in a
biological sample. (I) is used to determine whether a compound binds to
(I). A composition comprising (I) or a nucleic acid encoding (I), may be
used as a vaccine or diagnostic composition. The disease caused by
Streptococcus that is prevented or treated may be meningitis. Nucleic
acid encoding (I) may be used to recombinantly produce (I) and may be
used in gene therapy. Antibodies to (I) are used for affinity
chromatography, immunoassays, and distinguishing/identifying
Streptococcus proteins.

Sequence 118 AA;

Query Match 54.9%; Score 339; DB 23; Length 118;
Best Local Similarity 53.4%; Pred. No. 2.5e-34;
Matches 62; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

3 MIVGHGIDIEBELASIESAVTRHEGFRAKVLTAQEMERFTSLKGRQIEYLAGRWSAKEAF 62
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1 MIVGHGIDLQEIFSAIEKVYQXNRFFAQKITLQEALAIFFESPYYKRRLNYLAGRWSGKEAF 60

63 SKAMGTISKLGFODLEVLNNRGAPYFSQAPFSGKIMLSISHTDQFVTASVILLEE 118
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
61 AKAI GTIGRLTFODIELNDVRGCPILTKSPFKGNSTFISHSGNVVQASVILED 116

```

RESULT 8
AAY91289
ID AAY91289 standard; Protein; 119 AA.
XX
AC AAY91289;
XX
DT 30-MAY-2000 (first entry)
XX
DE Group B Streptococcus protein sequence SEQ ID NO:15.
XX
KW Group B Streptococcus; Streptococcus agalactiae; protein antigen;
KM vaccine; screening; immunogen; detection; diagnosis; infection;
KW antibody; affibody; antibacterial.
XX
OS Streptococcus agalactiae.
XX
PN WO200006736-A2.
XX
PD 10-FEB-2000.
XX
PF 27-JUL-1999; 99WO-GB02444.
XX
PR 27-JUL-1998; 98GB-0016335.
PR 19-MAR-1999; 99US-0125163.
XX
PA (MICR-) MICROBIAL TECHNICS LTD.
XX
PI Le Page RWF, Wells JM, Hannify SB;
DR WPI; 2000-195299/17.
XX
PT New Group B Streptococcus protein, useful as vaccine, for diagnosis of
PT Streptococcal infections and for screening of antibodies or affibodies
XX
PS Claim 1; Fig 1; 123pp; English.
XX
CC AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given
CC in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), also
CC known as Streptococcus agalactiae. The GBS polynucleotides and
CC polypeptides have antibacterial activity. Immunogenic compositions
CC comprising GBS polynucleotides or polypeptides can be used as vaccines
CC and for the treatment or prophylaxis of GBS infection. The
CC polynucleotides and polypeptides can also be used in the detection of GBS
CC and for screening DNA encoding bacterial cell envelope associated or
CC secreted antigens in gram positive bacteria. AAA05873 to AAA05941
CC represent primers used in the exemplification of the present invention.
XX
SQ Sequence 119 AA;

Query Match          53.2%; Score 328.5; DB 21; Length 119;
Best Local Similarity 52.1%; Pred. No. 5.3e-33;
Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY      3 MIVGHGIDIEELASIESAVTRHEGFAGKRVLTQAEMERFTSLKG-RRQI EYLGRWSAKEA 61
        |||||:::|:| |::|:|||| |:| :||:| |||:||||
Db      1 MIVGHGIDLQEILEAITKAYERNRQFAERVLTGEELLFSGISNPKRQMSFLTGRWAAKEA 60
QY      62 FSKAMGTGISKLGFODLEVLNNERGAPYFSQAFPSGKIWLISHTDQFVTASVIL EE 118
        :|||:|||| |:| |:|:|:~::~||| ::|||:| :|||:||||
Db      61 YSKALGTIGIKVNPHDIELSDDKGAPLITKEPFGKS FVSISHSGNYAQASVIL EE 117

RESULT 9
ABP27225
ID ABP27225 standard; Protein; 119 AA.
XX
AC ABP27225;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polypeptide SEQ ID NO 3626.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
```

KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
OS Streptococcus agalactiae.
XX WO200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001; 2001WO-GB04789.
XX PR 27-OCT-2000; 2000GB-0026333.
PR 24-NOV-2000; 2000GB-0028727.
PR 07-MAR-2001; 2001GB-0005640.
XX PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tettelin H;
XX DR MPI; 2002-352536/38.
DR N-PSDB; ABN67856.
XX PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX PS Claim 1; Page 3516; 4525pp; English.
XX CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX SQ Sequence 119 AA;
SQ Query Match 53.2%; Score 328.5; DB 23; Length 119;
Best Local Similarity 52.1%; Pred. No. 5.3e-33;
Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;
QY 3 MIVGHGIDIEELASIESAVTRHGFAPKRVLTQEMERFTSLKG-RQIEYLAGRWSAKKA 61
DB 1 MIVGHGIDIQEIEAITKAYERNRQFAERVLTEQELLLFKGISNPKQMSFLTGRWAAKKA 60
QY 62 FSKAMGTGISKLGFDLEVLNNERGAPYFSQAPFSGKIWLISHTDQFVTASVILEE 118
DB 61 YSKALGTGIGKVNPHDIEILSDDKGAPLITKEPFNGKSFVSIHSGNYAQASVILEE 117
RESULT 10
ID ABB54157 standard; Protein; 119 AA.
XX AC ABB54157;
XX DT 16-MAY-2002 (first entry)
DE Lactococcus lactis protein acpS.
XX

KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX Lactococcus lactis IL1403.
OS FR2807446-A1.
XX PN 12-OCT-2001.
XX PD 11-APR-2000; 2000FR-0004630.
XX PF 11-APR-2000; 2000FR-0004630.
XX PR 11-APR-2000; 2000FR-0004630.
XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX DR MPI; 2002-043418/06.
XX PT New nucleotide sequence useful in the identification or Lactococcus
PT lactis and related species -
XX PS Claim 6; SEQ ID No 859; 2504pp; French.
XX CC The present invention is related to a Lactococcus lactis nucleotide
CC sequence (ABA90521) and related proteins (ABBS3300-ABBS5621). The
CC nucleic acid sequence is useful in the detection and/or amplification of
CC nucleic acid sequence, particularly to identify Lactococcus lactis or
CC related species. The proteins of the invention are useful for the
CC biosynthesis or biodegradation of a composition of interest. The
CC invention helps research in lactic bacteria, particularly useful in the
CC production of yogurt and cheese.
CC Note: The sequence data for this patent is based on equivalent patent
CC WO200177334 (published 18-OCT-2001) which is available in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 119 AA;
SQ Query Match 48.9%; Score 302; DB 23; Length 119;
Best Local Similarity 51.3%; Pred. No. 1.1e-29;
Matches 61; Conservative 25; Mismatches 31; Indels 2; Gaps 2;
QY 3 MIVGHGIDIEELASIESAVTRHGFAPKRVLTQEMERFTSLKG-RQIEYLAGRWSAKKA 61
DB 1 MVFGTGVDNVELSRIQKALTRSERFVEQVLTAVLEKYNFSQSTARKTEFLAGRWAAKKA 60
QY 62 FSKAMGTGISK-LGFQDLEVLNNERGAPYFSQAPFSGKIWLISHTDQFVTASVILEEN 119
DB 61 FSKAYGTGFGKALGMHDLERKDELGKPFFTKHPFDGQVHLSISHSNLEAVAFVLEKN 119
RESULT 11
ID AAU35183 standard; Protein; 117 AA.
XX AC AAU35183;
XX DT 13-FEB-2002 (first entry)
XX DE Enterococcus faecalis cellular proliferation protein #470.
XX KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX OS Enterococcus faecalis.
XX XX WO200170955-A2.
XX PN 27-SEP-2001.
XX PD 21-MAR-2001; 2001WO-US09180.
XX PF 21-MAR-2001; 2000US-191078P.
XX PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR

PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR MPI; 2001-611495/70.
DR N-PSDB; AAS53042.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Example 3; Seq ID No 10776; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 117 AA;

Query Match 48.7%; Score 301; DB 22; Length 117;
Best Local Similarity 51.3%; Pred. No. 1.5e-29;
Matches 59; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAAQEMERFTSLKGRQIEYLAGRWSAKAFAF 62
Db 1 MIKIGIDAVELSRIKPIVEKQGSFIQRVLTLPNELTLFEKLSRKQIEFLAGRFACKAFAF 60

QY 63 SKAMGTGISKGFQDLEVLNNERGAPYFSQAPFSGKIWLISISHTDQFVTASVIL 117
Db 61 SKAMGTGIGKVGIDIEVLTEKTGAPYVANSBHNKGVFSITHTDTMAIAQIVLE 115

RESULT 12
ID AAY88389 standard; Protein; 121 AA.
AC AAY88389;
XX
DT 25-JUL-2000 (first entry)
XX
DE B-ydCB essential bacterial protein amino acid sequence.
XX
KW Bacterial gene; B-ydCB; Streptococcus pneumoniae; antibacterial compound;
KW acyl carrier protein synthase; identify; bacterial infection; treatment.
XX
OS Bacillus subtilis.
XX
PN WO200018952-A1.
PD 06-APR-2000.
XX

PF 30-SEP-1999; 99WO-US22666.
XX
PR 30-SEP-1998; 98US-0163446.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Fritz C, Youngman P, Guzman L;
XX
DR MPI; 2000-303457/26.
DR N-PSDB; AAA13271.
XX
PT Identifying new antibacterial agents particularly against Streptococcus
PT pneumoniae, uses S-ydCB polypeptide from S. pneumoniae and B-ydCB
PT polypeptide from Bacillus subtilis -
XX
PS Claim 17; Fig 2; 58pp; English.
XX
CC This sequence represents the essential bacterial protein B-ydCB from
CC Bacillus subtilis. B-ydCB is an ortholog of the S-ydCB from Streptococcus
CC pneumoniae. The gene encodes a protein which has structural
CC characteristics of acyl carrier protein synthase and displays synthase
CC activity in vitro. The protein is used in a method for identifying an
CC antibacterial agent, which comprises contacting an S-ydCB or B-ydCB
CC polypeptide with a test compound and detecting an interaction between the
CC polypeptide and the test compound, where the interaction indicates that
CC the compound is an antibacterial compound. Antibacterial agents
CC identified using the method may be used to treat a bacterial infection,
CC especially Streptococcus pneumoniae in mammals, especially a human or
CC rodent. The method can be configured for high throughput screening of
CC numerous candidate antibacterial agents, and identified agents should
CC have a broad spectrum of antibacterial activity.
XX
SQ Sequence 121 AA;

Query Match 40.6%; Score 251; DB 21; Length 121;
Best Local Similarity 44.6%; Pred. No. 2.9e-23;
Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAAQEMERFTSLKGRQIEYLAGRWSAKAFAF 62
Db 1 MIYGIDLTIELKRIASMAGRQKRFARILITRSELDQYELSEKRNPEFLAGRFACKAFAF 60

QY 63 SKAMGTGISK-LGFQDLEVLNNERGAPY-----FSQAPFSGKIWLISISHTDQFVTASVIL 116
Db 61 SKAFGTGIGRLSFDIDIEIRKDQNGKPYIICTKLSQA----AVHVSITHTKEYAAQAVI 116

QY 117 E 117
Db 117 E 117

RESULT 13
ID AAM52130 standard; protein; 121 AA.
AC AAM52130;
XX
DT 01-FEB-2002 (first entry)
XX
DE Bacillus subtilis ACPS.
XX
KW Bacillus subtilis; ACPS; acyl carrier protein synthase; active site;
KW protein coordinate data; CoA binding site; X-ray crystallography;
KW Swiss Protein P96618.
XX
OS Bacillus subtilis.
XX
PN WO200155340-A2.
PD 02-AUG-2001.
PF 26-JAN-2001; 2001WO-US02732.
XX

PR 28-JAN-2000; 2000US-178639P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Parris KD, Somers WS, Tam AS, Lin LL, Stahl ML;
 XX
 DR WPI; 2001-476201/51.
 XX
 PT Novel crystallized acyl carrier protein synthase enzyme used to
 PT identify an activator or inhibitor of a molecule or complex comprising
 PT a CoA binding site, and to determine the molecular structure of a
 PT molecule or complex -
 XX
 PS Disclosure; Fig 8; 181pp; English.
 CC The invention relates to a crystallized acyl carrier protein synthase
 CC (ACPS) enzyme used to identify an agent that interacts with the active
 CC site, to identify an activator or inhibitor of a molecule or molecular
 CC complex comprising a CoA binding site and to determine the molecular
 CC structure. The present sequence is that of the Bacillus subtilis ACPS.
 CC
 XX
 SQ Sequence 121 AA;
 Query Match 40.6%; Score 251; DB 22; Length 121;
 Best Local Similarity 44.6%; Pred. No. 2.9e-23;
 Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;
 QY 3 MIVGHGIDIEELASIESAVTRHGFPAKRVLTQEMERTSLKGRQIEYLAGRWSAKEAF 62
 Db 1 MIVGIGDITELKRIASMGROKRFARILTRSELDQYIELSEKRNFLAGRPAKEAF 60
 QY 63 SKAMGTGISK-LGFQDLEVLNNEGAPY----FSQAPFSGKIMLSISHTDQFVTASVIL 116
 Db 61 SKAFGTGIGRQLSFQDIEIRKQNGKPYIICTKLSQA----AVHVSITHTKETAAQAQVVI 116
 QY 117 E 117
 Db 117 E 117
 RESULT 14
 AAU10694
 ID AAU10694 standard; protein; 120 AA.
 XX
 AC AAU10694;
 XX
 DT 25-FEB-2002 (first entry)
 XX
 DE B. subtilis ACPS used to grow ACP/ACPS complex crystals.
 XX
 KW Crystal structure; acyl carrier protein synthase; acyl carrier protein;
 KW rational drug design method; antibiotic; 4'-phosphopantetheinyl; P-pant;
 KW ACP/ACPS complex; protein co-ordinate data.
 XX
 OS Bacillus subtilis.
 XX
 PN WO200185743-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 26-JAN-2001; 2001WO-US02949.
 XX
 PR 08-MAY-2000; 2000US-202466P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Parris KD, Somers WS, Tam AS, Lin LL, Stahl ML, Powers R, Xu G;
 XX
 DR WPI; 2002-055580/07.
 XX
 PT Crystallised complex useful in rational drug design methods, comprises

PT acyl carrier protein synthase and acyl carrier protein -
 XX
 PS Example 1; Fig 1; 147pp; English.
 XX
 CC The present invention relates to a crystallised structure comprising
 CC acyl carrier protein synthase (ACPS) complexed with acyl carrier
 CC protein (ACP). The invention also describes the solution structure
 CC of Bacillus subtilis ACP. Both these structures are useful in rational
 CC drug design methods for identifying agents that may interact with
 CC active sites of ACPS and ACP, and for testing these agents to identify
 CC agents that may represent novel antibiotics. They are also useful for
 CC design and selection of potent and selective agents which interact with
 CC ACPS and ACP, and for the design of antibiotics and other agents that
 CC interfere with 4'-phosphopantetheinyl (P-pant) attachment, thus
 CC preventing activation of corresponding carrier proteins. The present
 CC sequence represents B. subtilis ACPS used to grow ACP/ACPS complex
 CC crystals.
 CC
 XX
 SQ Sequence 120 AA;
 Query Match 39.3%; Score 243; DB 23; Length 120;
 Best Local Similarity 44.1%; Pred. No. 2.8e-22;
 Matches 52; Conservative 25; Mismatches 31; Indels 10; Gaps 3;
 QY 6 GHGIDIBELASIESAVTRHGFPAKRVLTQEMERTSLKGRQIEYLAGRWSAKEAFSKA 65
 Db 3 GIGDITELKRIASMGROKRFARILTRSELDQYIELSEKRNFLAGRPAKEAFPSKA 62
 QY 66 MGTGISK-LGFQDLEVLNNEGAPY----FSQAPFSGKIMLSISHTDQFVTASVILE 117
 Db 63 FGTGIGRQLSFQDIEIRKQNGKPYIICTKLSQA----AVHVSITHTKETAAQAQVVI 116
 RESULT 15
 ABB47581
 ID ABB47581 standard; Protein; 118 AA.
 XX
 AC ABB47581;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #285.
 XX
 KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 XX
 PN WO200177335-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 11-APR-2001; 2001WO-FR01118.
 XX
 PR 11-APR-2000; 2000FR-0004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 XX
 DR WPI; 2002-010914/01.
 XX
 PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and
 PT related polypeptides -
 XX

PS Claim 6; SEQ ID No 286; 192bp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 118 AA;

Query Match 37.7%; Score 233; DB 23; Length 118;
Best Local Similarity 42.7%; Pred. No. 5e-21;
Matches 50; Conservative 30; Mismatches 35; Indels 2; Gaps 2;
QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAEEMERFTSLKGRQTEYLAGRWSAKEAF 62
Db 1 MIKGIGLMDLDERVKQVEKNPRFIERVLTKEIKQFEKYEGRNRIEFLAGRFAAKEAY 60
QY 63 SKAMGTGISK-LGFQDLEVLNNEGAPYFSQAPFSGK-IWLSTSHTDQFVTASVILE 117
Db 61 AKANGTGFGRHLSFTDVEILQVEDGRPHVTLIPVKSGENVFVSIHTARSAAQVITE 117

Search completed: December 10, 2003, 19:35:09
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OM protein - protein search, using sw model

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Title: US-09-897-645-1

Perfect score: 618

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Maximum Match 100%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	618	100.0	122	3	US-08-987-144-2 Sequence 2, Appli
2	618	100.0	156	4	US-09-163-446-2 Sequence 2, Appli
3	289	46.8	129	4	US-09-107-532A-6990 Sequence 6990, Ap
4	251	40.6	121	4	US-09-163-446-4 Sequence 4, Appli
5	199.5	32.3	124	4	US-09-134-001C-4274 Sequence 4274, Ap
6	139.5	22.6	126	4	US-08-728-742A-10 Sequence 10, Appl
7	135.5	21.9	122	4	US-09-198-452A-330 Sequence 330, App
8	111.5	18.0	119	4	US-08-728-742A-11 Sequence 11, Appl
9	111.5	18.0	121	4	US-08-728-742A-2 Sequence 2, Appli
10	110	17.8	121	4	US-08-728-742A-3 Sequence 3, Appli
11	107.5	17.4	120	4	US-08-728-742A-1 Sequence 1, Appli
12	107	17.3	122	4	US-08-728-742A-4 Sequence 4, Appli
13	81	13.1	233	4	US-09-328-352-7929 Sequence 7929, Ap
14	80.5	13.0	208	4	US-09-134-001C-3478 Sequence 3478, Ap
15	76	12.3	130	4	US-08-728-742A-8 Sequence 8, Appli
16	74	12.0	130	4	US-08-728-742A-7 Sequence 7, Appli
17	72.5	11.7	371	4	US-09-134-001C-3672 Sequence 3672, Ap
18	72	11.7	169	4	US-09-107-532A-6366 Sequence 6366, Ap
19	71.5	11.6	130	4	US-08-728-742A-5 Sequence 5, Appli
20	71.5	11.6	431	4	US-09-107-532A-7056 Sequence 7056, Ap
21	71.5	11.6	475	4	US-09-252-991A-26219 Sequence 26219, A
22	70.5	11.4	318	3	US-08-680-506-3 Sequence 3, Appli
23	70.5	11.4	449	3	US-08-680-506-7 Sequence 7, Appli
24	70.5	11.4	1052	3	US-09-255-502-7 Sequence 7, Appli
25	70.5	11.4	1052	4	US-09-360-237-1 Sequence 1, Appli
26	70.5	11.4	1052	4	US-09-360-237-3 Sequence 3, Appli
27	68	11.0	113	4	US-09-107-532A-6985 Sequence 6985, Ap

28	66	10.7	176	4	US-09-252-991A-24888	Sequence 24888, A
29	66	10.7	518	4	US-09-134-001C-4348	Sequence 4348, Ap
30	65.5	10.6	348	4	US-09-325-932A-160	Sequence 160, App
31	65.5	10.6	970	6	5229293-2	Patent No. 5229293
32	65	10.5	359	4	US-09-252-991A-21741	Sequence 21741, A
33	64.5	10.4	248	4	US-09-325-932A-161	Sequence 161, App
34	64	10.4	514	4	US-09-252-991A-19394	Sequence 19394, A
35	64	10.4	812	4	US-09-166-350-12	Sequence 12, Appl
36	63.5	10.3	468	4	US-09-252-991A-17208	Sequence 17208, A
37	63.5	10.3	592	6	5200183-18	Patent No. 5200183
38	63	10.2	129	4	US-08-728-742A-6	Sequence 6, Appli
39	63	10.2	437	2	US-08-737-716-2	Sequence 2, Appli
40	62.5	10.1	258	4	US-09-328-352-4425	Sequence 4425, Ap
41	62.5	10.1	343	4	US-09-107-532A-6711	Sequence 6711, Ap
42	62.5	10.1	2154	2	US-08-841-349-4	Sequence 4, Appli
43	62	10.0	165	1	US-08-051-142-2	Sequence 2, Appli
44	62	10.0	539	4	US-09-198-452A-543	Sequence 543, App
45	62	10.0	587	1	US-08-844-280-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-987-144-2
; Sequence 2, Application US/08987144
; Patent No. 6060282
; GENERAL INFORMATION:
; APPLICANT: Rosteck Jr., Paul R.
; TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: U.S.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,144
; FILING DATE: December 8, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-11754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: 1linear
; MOLECULE TYPE: protein
; US-08-987-144-2
Query Match 100.0%; Score 618; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.7e-71;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRMIVGHGIDIEELASIESAVTRHGFAGKRVLTQAEMERFTSLKGRQIEYLAGRWSAKE 60
Db 1 MRMIVGHGIDIEELASIESAVTRHGFAGKRVLTQAEMERFTSLKGRQIEYLAGRWSAKE 60
QY 61 AFSKAMGTGISKLGFDLEVLNNRGAIFYSQAPFSGKIWTLSHTDQFVTASVILEENH 120
Db 61 AFSKAMGTGISKLGFDLEVLNNRGAIFYSQAPFSGKIWTLSHTDQFVTASVILEENH 120

QY 121 ES 122
Db 121 ES 122

RESULT 2

US-09-163-446-2
; Sequence 2, Application US/09163446
; Patent No. 6515119
; GENERAL INFORMATION:
; APPLICANT: Fritz, Christian
; APPLICANT: Youngman, Philip
; APPLICANT: Guzman, Luz-Maria
; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
; FILE REFERENCE: 07334/097001
; CURRENT APPLICATION NUMBER: US/09/163,446
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Streptococcus pneumonia
US-09-163-446-2

Query Match 100.0%; Score 618; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 9.6e-71;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMIVGHGIDIEELASIESAVTRHGFARVLTQAEMERFTSLKGRQIEYLAGRWSAKE 60
Db 35 MRMIVGHGIDIEELASIESAVTRHGFARVLTQAEMERFTSLKGRQIEYLAGRWSAKE 94

QY 61 AFSKAMGTGISKLGFDLEVLNNGGAPYFSQAPFSGKIWLISHTDQFVTASVILENH 120
Db 95 AFSKAMGTGISKLGFDLEVLNNGGAPYFSQAPFSGKIWLISHTDQFVTASVILENH 154

QY 121 ES 122
Db 155 ES 156

RESULT 3

US-09-107-532A-6990
; Sequence 6990, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:

US-09-107-532A-6990
; Sequence 6990, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6990:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...129

SEQUENCE DESCRIPTION: SEQ ID NO: 6990:

US-09-107-532A-6990

Query Match 46.8%; Score 289; DB 4; Length 129;
Best Local Similarity 48.3%; Pred. No. 5.1e-29;
Matches 56; Conservative 21; Mismatches 39; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESAVTRHGFARVLTQAEMERFTSLKGRQIEYLAGRWSAKEAF 62
Db 14 MIVGHGIDIEELASIESAVTRHGFARVLTQAEMERFTSLKGRQIEYLAGRWSAKEAF 73

QY 63 SKAMGTGISKLGFDLEVLNNGGAPYFSQAPFSGKIWLISHTDQFVTASVILENH 118
Db 74 SKAMGTGISKLGFDLEVLNNGGAPYFSQAPFSGKIWLISHTDQFVTASVILENH 129

RESULT 4

US-09-163-446-4
; Sequence 4, Application US/09163446
; Patent No. 6515119
; GENERAL INFORMATION:
; APPLICANT: Fritz, Christian
; APPLICANT: Youngman, Philip
; APPLICANT: Guzman, Luz-Maria
; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
; FILE REFERENCE: 07334/097001
; CURRENT APPLICATION NUMBER: US/09/163,446
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Streptococcus pneumonia
US-09-163-446-4

Query Match 40.6%; Score 251; DB 4; Length 121;
Best Local Similarity 44.6%; Pred. No. 3.2e-24;
Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;

QY 3 MIVGHGIDIEELASIESAVTRHGFARVLTQAEMERFTSLKGRQIEYLAGRWSAKEAF 62
Db 1 MIVGHGIDIEELASIESAVTRHGFARVLTQAEMERFTSLKGRQIEYLAGRWSAKEAF 60

QY 63 SKAMGTGISKLGFDLEVLNNGGAPYFSQAPFSGKIWLISHTDQFVTASVILENH 116
Db 61 SKAMGTGISKLGFDLEVLNNGGAPYFSQAPFSGKIWLISHTDQFVTASVILENH 116

QY 117 E 117
Db 117 E 117

RESULT 5

US-09-134-001C-4274

; Sequence 4274, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4274
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4274

Query Match 32.3%; Score 199.5; DB 4; Length 124;
Best Local Similarity 37.2%; Pred. No. 1.2e-17;
Matches 45; Conservative 30; Mismatches 41; Indels 5; Gaps 4;

QY 1 MRNIVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEMERFTSLKG-RRQIEYLAGRWSAK 59
Db 6 IQVIVGIGIDILEIERIKN-LQNQTKFIERILTEERDKLNQYTNQRRLEFLAGRFTVK 64
QY 60 EAFSKAMGTGISK-LGFQDLEVLNNERGAPYFSQAPFSGKIWLISHTDQFVTASVILEE 118
Db 65 EAFSKALGTGLGKSVSFQDINCYNDAIGKPCIDYPGFYTHV--SITHTENYAMSQVILEK 122
QY 119 N 119
Db 123 N 123

RESULT 6

US-08-728-742A-10
; Sequence 10, Application US/08728742A

; Patent No. 6579695

; GENERAL INFORMATION:

; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals

; TITLE OF INVENTION: PHOSPHOPANTETHEINYL TRANSFERASES AND USES THEREOF

; NUMBER OF SEQUENCES: 78

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/728,742A

; FILING DATE: October 11, 1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/005,152

; FILING DATE: October 13, 1995

; APPLICATION NUMBER: 60/021,650

; FILING DATE: July 12, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Amy E. Mandragouras

; REGISTRATION NUMBER: 36,207

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-728-742A-10

Query Match 22.6%; Score 139.5; DB 4; Length 126;
Best Local Similarity 30.3%; Pred. No. 5.1e-10;
Matches 40; Conservative 26; Mismatches 39; Indels 27; Gaps 5;

QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEMERFTSLKGRQIEYLAGRWSAKEAF 62
Db 3 ILGLTDIVEIARIIEAVIARSGDRLARRVLSDNEMAIWKT--HQPVRFIAKFAVKEAA 60
QY 63 SKAMGTGI-SKLGFDLEVLNNERGAPYFSQAPFSGKIWLISHTDQFVTASVILEE 105
Db 61 AKAFGTGIRNGLAFNQNQFEVFNDELGKPRLL-----RLWGEALKLAELGVANMHVTLAD 113
QY 106 TDQFVTASVILE 117
Db 114 ERHYACATVILE 125

RESULT 7

US-09-198-452A-330
; Sequence 330, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffiths, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 330

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-330

Query Match 21.9%; Score 135.5; DB 4; Length 122;
Best Local Similarity 35.3%; Pred. No. 1.6e-09;
Matches 42; Conservative 19; Mismatches 49; Indels 9; Gaps 5;

QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEMERFTSLKGRQIEYLAGRWSAKEAF 62
Db 3 IHHGTDIEISRIIEAIAIHGNRLNRIFT--EAEQYCLEKTDPIPSFAGRFAGKEAV 60
QY 63 SKAMGTGI-SKLGFDLEVLNNERG---APYFSQAPFS-GKIWLISHTDQFVTASVI 115
Db 61 AKALGTGIGSVVAMKDIEVFVSHGPEVLLPSHVYAKIGISKVILSISHCKEYATATAI 119

RESULT 8

US-08-728-742A-11

; Sequence 11, Application US/08728742A

; Patent No. 6579695

; GENERAL INFORMATION:

; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals

; TITLE OF INVENTION: PHOSPHOPANTETHEINYL TRANSFERASES AND USES THEREOF

; NUMBER OF SEQUENCES: 78

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:


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1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: PatentIn Release #1.0, Version #1.25
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/728,742A
7 FILING DATE: October 11, 1996
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 60/005,152
10 FILING DATE: October 13, 1995
11 APPLICATION NUMBER: 60/021,650
12 FILING DATE: July 12, 1996
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Amy E. Mandragouras
15 REGISTRATION NUMBER: 36,207
16 REFERENCE/DOCKET NUMBER: HMT-015
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (617)227-7400
19 TELEFAX: (617)742-4214
20 INFORMATION FOR SEQ ID NO: 11:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 119 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 MOLECULE TYPE: peptide
26 FRAGMENT TYPE: internal
27
28 US-08-728-742A-11

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Query Match          18.0%; Score 111.5; DB 4; Length 119;  
Best Local Similarity 32.5%; Pred. No. 1.7e-06;  
Matches    40; Conservative   22; Mismatches   40; Indels    21; Gaps     8;
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Db 6 GHGIDIEELASIESAVTRHEGFARVLTAGEMERFTSLKGRROIEYLAGRWSAKEAFSKA 65
| : | : | : | : | : | : | : | : | : | : | : | : | : | :
2 GGVVDVELITSIN---VENDTFIERNFTPOETI-YCSAQPSVOSSF-AQTWSAKEAVFKS 56

Qy 66 MGTSISKLG-----FODLEVLNNRGAPFYF-----SQAPFSG--KIWLSISHTD-QFVT 111
: | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 57 L-GVKSLGGALKKDIEIVRVKNKNAFAVELHGNAKKAEEAGTVDVKSISHDDLQAVA 114

112 ASV 114
:
Db 115 VAV 117

RESULT 9
US-08-728-742A-2
; Sequence 2, Application US/08728742A
; Patent No. 6579695
; GENERAL INFORMATION:
; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
; TITLE OF INVENTION: PHOSPHOPANTETHEINYL TRANSFERASES AND USES THEREOF
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,742A
; FILING DATE: October 11, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,152
; FILING DATE: October 13, 1995
; APPLICATION NUMBER: 60/021,650
; FILING DATE: July 12, 1996

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Amy E. Mandragouras
;   REGISTRATION NUMBER: 36,207
;   REFERENCE/DOCKET NUMBER: HMI-015
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 227-7400
;   TELEFAX: (617) 742-4214
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 121 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FRAGMENT TYPE: internal
US-08-728-742A-2

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	Query Match	Similarity	18.0%;	Score	111.5;	DB	4;	Length	121;
	Best Local	Similarity	32.5%;	Pred.	No.	1.8e-06;			
	Matches	Conservative	22;	Mismatches	40;	Indels	21;	Gaps	8;
OY	6	GHGIDIFELASTESAVTRHEGFAKRVLTAQEMERFTSLKGRQIEYLAGRWSAKEAFSKA	65						
Db	2	GVGDVDELITSIN---VENDTFIERNFTPQEIE.YCSAQPSVQSSF-AGTWSAKEAVFKS	56						
OY	66	MGTGISKLG----FQDLEVLNNERGAPYF-----SQAPFSG--KIWLISHTD-QFYVT	111						
Db	57	L-GVKSLGGGALKDIEIVRVKNKPAVELHGNAKKAEEAGVTDVKVISISHDDLQAIVA	114						
OY	112	ASV	114						
Db	115	VAV	117						

RESULT 10
 US-08-728-742A-3
 ; Sequence 3, Application US/08728742A
 ; Patent No. 6579695
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
 ; TITLE OF INVENTION: PHOSPHOPANTHEINYL TRANSFERASES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 78
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/728,742A
 ; FILING DATE: October 11, 1996
 ;
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/005,152
 ; FILING DATE: October 13, 1995
 ; APPLICATION NUMBER: 60/021,650
 ; FILING DATE: July 12, 1996
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amy E. Mandragouras
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: HMT-015
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 121 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-728-742A-3

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Query Match	17.8%;	Score 110;	DB 4;	Length 121;
Best Local Similarity	30.3%;	Pred. No. 2.7e-06;		
Matches	36;	Conservative	19;	Mismatches 48;
			Indels	16;
			Gaps	5;

[illegible]

RESULT 11
US-08-728-742A-1
; Sequence 1, Application US/08728742A

```

; GENERAL INFORMATION:
;
; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
;
; TITLE OF INVENTION: PHOSPHOPANTETHEINYL TRANSFERASES AND USES THEREOF
;
; NUMBER OF SEQUENCES: 78
;
; CORRESPONDENCE ADDRESS:
;

```

ADDRESS: LAHIVE & COCKFIELD, LLC
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/005,152
 FILING DATE: October 13, 1995
 APPLICATION NUMBER: 60/021,650
 FILING DATE: July 12, 1996
 ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-015
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEO ID NO: 1

SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide

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; FRAGMENT TYPE: internal
US-08-728-742A-1

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1980

Query Match	17.4%;	Score 107.5;	DB 4;	Length 120;
Best Local Similarity	32.3%;	Pred. No. 5.6e-06;		
Matches	40;	Conservative	15;	Mismatches 52;
			Indels	17;
			Gaps	6;

DQ
6 GHGIDIELLASIESAVTRHEGFRAKRVLTAGEMEFPTSLKGRROIETLAGRWSAKAEASKA 65

Dd
2 GVGVDVETLLSAIN--IDNETFIERNFTGNEVE--YCLNTAHQAQSFSTGTGSAAKEAVPKA 56

66 MGNGISKLGQ--DLEVLNNEKGAPYF-----SQAPFSG--KIMLSISHTDQFVTASV 114
:
57 LGVESKGAGASLIDIEITRDVNGAPKVILHGEAKKAAGAkvNVNISISH-DDFQATAV 115

QY	115	116	117	118
Db	116	117	118	119

RESULT 12
US-08-728-742A-4

Sequence 4, Application US/08728742A
Patent No. 6579695
GENERAL INFORMATION:
APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wall
TITLE OF INVENTION: PHOSPHOPANTETHEINYL TRANSFERASES AND USES THEREOF
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 13, 1995

; FILING DATE: JULY 12, 1999
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amy E. Mandragouras
 ; REGISTRATION NUMBER: 36

REFERENCE/DOCKET NUMBER: HMI-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

```
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;

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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-728-742A-4

```

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Query Match      17.3%; Score 107; DB 4; Length 122;
Best Local Similarity 32.7%; Pred. No. 6.7e-06;
Matches 37; Conservative 19; Mismatches 37; Indels 20; Gaps 6;

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OY      8 GIDIEELASIESAVTRHEGFAKRVLTAEEMERFTSLKGRQIEYLGRWSAKAFAFRMG 677
        ||:||::|| :||| :||| |::||| ||||| ||||| ::
Db      6 GVDVELVSAIS---IDNETFIERNFT--DTERKXCFAAPNPQASFAGRWSAKEAFVSIL- 59
```

```

QY      68 TGISKUG-----FQDLEVLNNERGAPYF-----SQAPFSG-KIMLSISHTD 107
      |||      :|:|:|:|      |||      |      :|:|:|:|
Dd      60 -GISGCAAPLKDIEIISSESGAPEVVLHGEAKAATTAGVKSVSISHTD 111

```

RESULT 13
US-09-328

; Sequence 7929, Application US/09328352
; Patent No. 6562958

; GENERAL INFORMATION;

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRED: 05000 0000

FILE REFERENCE: G1C99-03FA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 19:33:16 ; Search time 20 Seconds
(without alignments)
586.629 Million cell updates/sec

Title: US-09-897-645-1
Perfect score: 618

Sequence: 1 MRNVGHGIDIEELASIESA.....ISHTDQFVTASVILEENHES 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608	98.4	120	2	H95197
2	608	98.4	120	2	D98064
3	302	48.9	119	2	C86730
4	279	45.1	119	2	F83714
5	251	40.6	121	1	H69772
6	233	37.7	118	2	AE1185
7	228	36.9	118	2	AD1543
8	208	33.7	119	2	E89999
9	187.5	30.3	126	2	F82072
10	181	29.3	126	2	F71662
11	172.5	27.9	169	2	B72345
12	171	27.7	131	2	A97810
13	169.5	27.4	124	2	B96960
14	151.5	24.5	125	2	D81833
15	149.5	24.2	126	2	AG0828
16	148.5	24.0	126	2	E91057
17	148.5	24.0	126	2	B85902
18	146.5	23.7	125	2	F81197
19	145.5	23.5	126	2	F84959
20	140	22.7	125	2	F71276
21	139.5	22.6	126	1	B42294
22	137.5	22.2	126	2	AF0356
23	135.5	21.9	122	2	D90789
24	135.5	21.9	122	2	A86530
25	135.5	21.9	122	2	B72093
26	135.5	21.9	122	2	G85649
27	133	21.5	115	2	A81286
28	128.5	20.8	115	2	G82895
29	125.5	20.3	119	2	C71556

30	125.5	20.3	191	2	AC3413	holo-[acyl-carrier
31	123	19.9	119	1	S73864	hypothetical prote
32	122.5	19.8	134	2	AH2703	holo-[acyl-carrier
33	122.5	19.8	134	2	H97485	holo-acyl-carrier
34	121.5	19.7	119	1	H64620	holo-[acyl-carrier
35	117.5	19.0	119	2	G71894	holo-[acyl-carrier
36	113	18.3	124	2	B70101	holo-acyl-carrier
37	111.5	18.0	125	2	D81710	holo-[acyl-carrier
38	111.5	18.0	1887	2	S61703	holo-acyl-carrier
39	110	17.8	1857	1	S01787	fatty-acid synthas
40	109	17.6	133	2	F75544	probable holo-acyl
41	108.5	17.6	133	2	E87442	holo-[acyl-carrier
42	108	17.5	123	2	T35573	probable holo-lacy
43	107.5	17.4	1885	1	JC4086	fatty-acid synthas
44	107	17.3	377	2	T43037	probable fatty-aci
45	107	17.3	1842	2	T43409	probable fatty-aci

ALIGNMENTS

RESULT 1

H95197
holo-[acyl-carrier protein] synthase [imported] - Streptococcus pneumoniae (strain TIG
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C/Accession: H95197
R/Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; He
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morriso
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: H95197
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-120 <KUR>
A/Cross-references: GB:AE005672; PIDN:AAK75777.1; PID:g14973193; GSPDB:GN00164; TIGR:S
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP1699
C/Superfamily: holo-ACP synthase

Query Match 98.4%; Score 608; DB 2; Length 120;
Best local Similarity 100.0%; Pred. No. 8.3e-56;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRYLTAQEMERFTSLKGRQIEYLGRWSAKEAF 62

Db 1 MIVGHGIDIEELASIESAVTRHEGFAKRYLTAQEMERFTSLKGRQIEYLGRWSAKEAF 60

QY 63 SKAMGTGISKLGFDLEVLNNERGAPYFSQAPFSQKIWLISHTDQFVTASVILEENHES 122

Db 61 SKAMGTGISKLGFDLEVLNNERGAPYFSQAPFSQKIWLISHTDQFVTASVILEENHES 120

RESULT 2

D98064
holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) [imported] - Streptococcus pneumonia

C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001

C/Accession: D98064
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Uaskunas, S.R

A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: D98064
A/Status: preliminary
A/Molecule type: DNA

Nature 396, 133-140, 1998
A/Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
A/Reference number: A71630; MUID:99039499; PMID:9823893
A/Accession: F71662
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-126 <AND>
A/Cross-references: GB:AJ235272; GB:AJ235269; NID:G3861033; PIDN:CAA15024.1; PID:G386112
A/Experimental source: strain Madrid E
C/Genetics:
A/Gene: acpS; RP577
C/Superfamily: holo-ACP synthase
C/Keywords: coenzyme A; transferase

	Query Match	29.3%;	Score 181;	DB 2;	Length 126;	
	Best Local Similarity	37.8%;	Pred. No. 1.5e-11;			
	Matches	48;	Conservative	25;	Mismatches	42;
					Indels	12;
					Gaps	5;
QY	3 MIVGHGIDIEELASIESAVTRH-EGFAKRVLTQAQEMERFTSLKGRQI EYLAGRWSAKEA	61				
Dd	1 MLIGVGTDIVQIPRIEKILNTYQELFPAKKILALKEKQFTLNNKTNHATFLAKRFSAKEA	60				
QY	62 FSKAMGTGISK-LGFQDLEVLNNERGAP-----YFSQ-AFPSGKIWLISHTDQVTA	112				
Dd	61 VSKAFGVGIGRGINFKDITINDNLGKPTVEISSHYTNKLAPFN--IHLSLSDYPICIA	118				
QY	113 SVILEEN	119				
Dd	119 FAITEEN	125				

RESULT 11
B72345
holo-(acyl carrier protein) synthase - *Thermotoga maritima* (strain MSB8)
C;Species: *Thermotoga maritima*
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: B72345
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <ARN>
A;Cross-references: GB:AE001741; GB:AE000512; NID:g4981208; PIDN:AD35774.1; PID:g498121
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0692

	Query Match	27.9%;	Score 172.5;	DB 2;	length 169;
	Best Local Similarity	38.4%;	Pred. No. 1.6e-10;		
	Matches	48;	Conservative	22;	Mismatches 30; Indels 25; Gaps 6;
QY	3 MIVGHGIDIEELASIESAVTRHEGFAGKRVLTQAQEMERFTSLKGRROI EYLAGRWSAKAEAF	62			
Db	1 MIVGVGIDVLEVERVP-----EKFAERILGSESEKRLFLTKRRR--EFIAGRFPALKEAF	52			
QY	63 SKAMGTGISKLGFQDLEVLNNRGAP-----YFSQAPSPSGKIWLISISHTDQFVTAS	113			
Db	53 FKALGTGLNGHSFTDVEFLS-NGKPVLVCVKHDFGFFNYA-----HVSLSH-DRFAYAL	104			
QY	114 VILEE	118			
Db	105 VVLEK	109			

RESULT 12
A97810
hypothetical protein acps [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: A97810
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: A97810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL03419.1; PID:g15619986; GSPDB:GN00173
C;Genetics: acps
A;Gene: acps
C;Superfamily: holo-ACP synthase

[illegible]

RESULT 13
B96960
holo-acyl-carrier protein synthase [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C/Accession: B96960
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Le
. J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genom Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: B96960
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-124 <KUR>
A/Cross-references: GB:AE001437; PIDN:AAK78469.1; PID:g15023349; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC0489
C/Superfamily: holo-ACP synthase

	Query Match	27.4%;	Score 169.5;	DB 2;	length 124;
	Best Local Similarity	33.9%;	Pred. No. 2.3e-10;		
	Matches	42;	Conservative 30;	Mismatches 41;	Indels 11; Gaps 3;
QY	3 MIVGHGIDIEELASIESAVTRHEGFARVLTQAEMERFTSLKGRQIEYLGRWSAKEAF	62			
	: : : : : : : : : : : : : : :				
Db	1 MIKGVGVDIIENRVKNALDRNYKFIEKLFSRREIAYIKAEKTKAQ--YIAGRFSAKEAV	58			
	: : : : : : : : : : : : : : :				
QY	63 SKAMGTGISKLGFQDLEVLNNERGAPYF-----SQAPPFG----KIMLSISHTDQFVTAS	113			
	: : : : : : : : : : : : : : :				
Db	59 SKALGTGRGFSFKNIETHKDDLGPPIVVLNGGARATAEGYGKYQVQLSISHDREKAIAAY	118			
	: : : : : : : : : : : : : : :				
QY	114 VILE	117			
	: :				
Db	119 AVLE	122			

RESULT 14
D81833
holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) **NMA2033** [imported] - *Neisseria meningitidis*

C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: D81833
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81833
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <PAR>
A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85252.1; PID:g738066
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: acps; NMA2033
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A; transferase

Query Match 24.5%; Score 151.5; DB 2; Length 125;
Best Local Similarity 33.9%; Pred. No. 1.7e-08;
Matches 43; Conservative 25; Mismatches 46; Indels 13; Gaps 4;

QY 3 MIVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEMERFTSLKGRQIEYLAGRWSAKEA 61
Db 1 MIVGIGTDIVSLKRIIVRLSKKFGQAFARILTPBELLEFF--QAGKPVNYLAKRFAAKEA 58
QY 62 FSKAMGTGI-SKLGFDLEVLNNERGAPYFSQAPFSGK-----IWLISHTDQFVT 111
Db 59 FAKAVGTGIRGAVSFRNTGIGHDALGKPEFFYAPALSKWLEEGGISRVSLSMSDEEDTVL 118
QY 112 ASVILEE 118
Db 119 AFAVAEK 125

RESULT 15
AG0828
holo-[acyl-carrier protein] synthase (EC 2.7.8.7) [imported] - Salmonella enterica subsp
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0828
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0828
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-126 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02779.1; PID:g16503789; GSPDB:GN00176
C;Genetics:
A;Gene: STY2823
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A; transferase

Query Match 24.2%; Score 149.5; DB 2; Length 126;
Best Local Similarity 33.3%; Pred. No. 2.8e-08;
Matches 44; Conservative 24; Mismatches 37; Indels 27; Gaps 6;

QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEMERFTSLKGRQIEYLAGRWSAKEAF 62
Db 3 ILGLGTDIVEIARIEAVISRSGERLARRVLSDNEMAIWET--HQQPVRFLLAKRPAVKEAA 60
QY 63 SKAMGTGI-SKLGFDLEVLNNERGAPYFSQAPFSGKIW-----LSISHTD----- 107
Db 61 AKAFGTGIRNGIAFNQFEVFNDELGKPRLL-----RLWGEALTIAEKLGVAHMHVTLAD 113
QY 108 --QFVTASVILE 117

Db 114 ERHYACATVILE 125
Search completed: December 10, 2003, 19:36:56
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 19:32:01 ; Search time 13 Seconds
(without alignments)

441.328 Million cell updates/sec

Title: US-09-897-645-1

Perfect score: 618

Sequence: 1 MEMVGHGIDIEELASIESA.....ISHTDQFVTASVILENHES 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608	98.4	120	1	ACPS_STRPN
2	397	64.2	119	1	ACPS_STRMU
3	339	54.9	118	1	ACPS_STRPY
4	339	54.9	118	1	ACPS_STRPY
5	328.5	53.2	119	1	ACPS_STRPY
6	302	48.9	119	1	ACPS_STRPY
7	279	45.1	119	1	ACPS_STRPY
8	278.5	45.1	119	1	ACPS_STRPY
9	251	40.6	121	1	ACPS_STRPY
10	233	37.7	118	1	ACPS_STRPY
11	228	36.9	118	1	ACPS_STRPY
12	221	35.8	117	1	ACPS_STRPY
13	212	34.3	119	1	ACPS_STRPY
14	210.5	34.1	126	1	ACPS_STRPY
15	208	33.7	119	1	ACPS_STRPY
16	199.5	32.3	117	1	ACPS_STRPY
17	199.5	32.3	122	1	ACPS_STRPY
18	196.5	31.8	117	1	ACPS_STRPY
19	195.5	31.6	126	1	ACPS_STRPY
20	189.5	30.7	133	1	ACPS_STRPY
21	187.5	30.3	136	1	ACPS_STRPY
22	181	29.3	126	1	ACPS_STRPY
23	176	28.5	139	1	ACPS_STRPY
24	172.5	27.9	169	1	ACPS_STRPY
25	171	27.7	131	1	ACPS_STRPY
26	169.5	27.4	124	1	ACPS_STRPY
27	159.5	25.8	126	1	ACPS_STRPY
28	158.5	25.6	127	1	ACPS_STRPY
29	151.5	24.5	125	1	ACPS_STRPY
30	150.5	24.4	127	1	ACPS_STRPY
31	149.5	24.2	125	1	ACPS_STRPY
32	148.5	24.0	125	1	ACPS_STRPY
33	148.5	24.0	125	1	ACPS_STRPY

34	148.5	24.0	128	1	ACPS_BUCBP
35	147	23.8	114	1	ACPS_MYCGE
36	146.5	23.7	125	1	ACPS_NEIME
37	145.5	23.5	126	1	ACPS_BUCAI
38	140	22.7	125	1	ACPS_TREPA
39	139.5	22.6	125	1	ACPS_ECOLI
40	138.5	22.4	137	1	ACPS_RHILLO
41	137.5	22.2	126	1	ACPS_YERPE
42	135.5	21.9	122	1	ACPS_CHUPN
43	135.5	21.9	122	1	ACPS_ECO57
44	133	21.5	115	1	ACPS_CAMJE
45	128.5	20.8	115	1	ACPS_UREPA

ALIGNMENTS

RESULT 1
ACPS_STRPN
ID ACPS_STRPN STANDARD; PRT; 120 AA.
AC Q9F7T5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR SP1699 OR SPRI541.
OS Streptococcus pneumoniae, and
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313, 171101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-255 / R6;
RX MEDLINE=20469436; PubMed=10903317;
RA McAllister K.A., Peery R.B., Meier T.I., Fischl A.S., Zhao G.;
RT "Biochemical and molecular analyses of the streptococcus pneumoniae
RT acyl carrier protein synthase, an enzyme essential for fatty acid
RT biosynthesis.";
RL J. Biol. Chem. 275:30864-30872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tetteijn H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Anglucci S., Dickinson T., Hickey E.K.,
RA Holt I.B., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-255 / R6;
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz R.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., Mcleaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH 3'-5'-ADP.

```

RX MEDLINE=20490359; PubMed=11032795;
RA Chirgadze N.Y., Briggs S.L., McAllister K.A., Fischl A.S., Zhao G.;
RT "Crystal structure of Streptococcus pneumoniae acyl carrier protein
RT synthase: an essential enzyme in bacterial fatty acid biosynthesis.";
RL EMBL J. 19:5281-5287(2000).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AF276617; AAG22706.1; -
DR EMBL; AE007463; AAK75777.1; -
DR EMBL; AE008522; AAL00345.1; -
DR PIR; D98064; D98064.
DR PIR; H95197; H95197.
DR PDB; 1FTE; 12-SEP-01.
DR PDB; 1FTF; 12-SEP-01.
DR PDB; 1FTH; 12-SEP-01.
DR TIGR; SPL699; -.
DR HAMAP; MF_00101; -; 1.
DR InterPro; IPR002582; ACPS.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMS; TIGR00516; acps; 1.
DR TIGRFAMS; TIGR00556; pantethn_trn; 1.
DR TIGRFAMS; TIGR00556; pantethn_trn; 1.
KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW 3D-structure; Complete proteome.
FT METAL
FT METAL
SQ SEQUENCE 120 AA; 13388 MW; 7FFB1848AC63DAEE CRC64;

Query Match 98.4%; Score 608; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 6,1e-54;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEBLASIESAVTRHEGFAKRVLTAEEMERTSLKGRROI EYLAGRWSAKAF 62
Db 1 MIVGHGIDIEBLASIESAVTRHEGFAKRVLTAEEMERTSLKGRROI EYLAGRWSAKAF 60

QY 63 SKAMGTGISKLGFDLEVLNNGAPYFSQAPFSGKIWLSISHTDQFVTASVILEENHES 122
Db 61 SKAMGTGISKLGFDLEVLNNGAPYFSQAPFSGKIWLSISHTDQFVTASVILEENHES 120

RESULT 2
ACPS_STRMU STANDARD; PRT; 119 AA.
ID ACPS_STRMU
AC Q8DSF3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR SMU.1835.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
```

```

RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE015010; AAN59458.1; -
DR HAMAP; MF_00101; -; 1.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMS; TIGR00516; acps; 1.
DR TIGRFAMS; TIGR00556; pantethn_trn; 1.
DR TIGRFAMS; TIGR00556; pantethn_trn; 1.
KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW Complete proteome.
FT METAL
FT METAL
SQ SEQUENCE 119 AA; 13218 MW; 450139C210FEF866 CRC64;

Query Match 64.2%; Score 397; DB 1; Length 119;
Best Local Similarity 62.7%; Pred. No. 7e-33;
Matches 74; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEBLASIESAVTRHEGFAKRVLTAEEMERTSLKGRROI EYLAGRWSAKAF 62
Db 1 MIVGHGIDLEDAVQRAHERSSRFASKVLTFKELIFTSKGRQVEYLAGRWSAKAF 60

QY 63 SKAMGTGISKLGFDLEVLNNGAPYFSQAPFSGKIWLSISHTDQFVTASVILEENH 120
Db 61 SKAYSGIGSLRFQDLIELANNKGAPIFTKSPFSGNIFISHSKNYVEASVILEENN 118

RESULT 3
ACPS_STRP3 STANDARD; PRT; 118 AA.
ID ACPS_STRP3
AC Q8NZK3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR SPYM3_1564 OR SP80303 OR SPYM18_1872.
OS Streptococcus pyogenes (serotype M3).
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466, 186103;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=MGAS315 / Serotype M3;
RC MEDLINE=22133808; PubMed=12122206;
RX Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
```

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RA Schliewert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ST-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes ST-1, SF370 and MGAS8232."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-biphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AB014166; AAM80171.1; -.
DR EMBL; AP005142; BAC63398.1; -.
DR EMBL; AE010093; AAL98380.1; -.
DR HAMAP; MF_00101; -.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_tmn.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantethn_tmn; 1.
KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW Complete proteome.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 118 AA; 13262 MW; 5AFE6F7EE64BDBC CRC64;

Query Match 54.9%; Score 339; DB 1; Length 118;
Best Local Similarity 53.4%; Pred. No. 4.3e-27;
Matches 62; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESAVTRHEGFARVLTQAQEMERFTSLKGRQIEYLAGRWSAKAF 62
Db 1 MIVGHGIDIEELASIEKVYQNRPRFAQKILTEQELAFESFPYKRRLNYLAGRWSGKEAF 60

QY 63 SKAMGTGISKLGFDLEVLNNRGAFFPSQAPFSGKIMLSISHTDQFTASVILEE 118
Db 61 AKATGTGIRLTFQDIEILNDVRCGPILTKSPFKGNSFISISHSNGNYQASVILEE 116

RESULT 4
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ACPS_STRPY
ID ACPS_STRPY STANDARD; PRT; 118 AA.
AC Q99Y97;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR SPY1804.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-biphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE006607; AAK34533.1; -.
DR HAMAP; MF_00101; -.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_tmn.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantethn_tmn; 1.
KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW Complete proteome.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 118 AA; 13289 MW; C3E45C5EBE64AC5D CRC64;

Query Match 54.9%; Score 339; DB 1; Length 118;
Best Local Similarity 53.4%; Pred. No. 4.3e-27;
Matches 62; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESAVTRHEGFARVLTQAQEMERFTSLKGRQIEYLAGRWSAKAF 62
Db 1 MIVGHGIDIEELASIEKVYQNRPRFAQKILTEQELAFESFPYKRRLNYLAGRWSGKEAF 60

QY 63 SKAMGTGISKLGFDLEVLNNRGAFFPSQAPFSGKIMLSISHTDQFTASVILEE 118
Db 61 AKATGTGIRLTFQDIEILNDVRCGPILTKSPFKGNSFISISHSNGNYQASVILEE 116

RESULT 5
ACPS_STR3
ID ACPS_STR3 STANDARD; PRT; 119 AA.
AC Q8E3M8; Q8DY09;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
DE ACPS OR GBS1729 OR SAG1685.
OS Streptococcus agalactiae (serotype III), and
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495, 216466;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tetteijn H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madup R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
RN [3]
RP FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
RN A to a Ser of acyl-carrier protein (By similarity).
CC -! CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -! COFACTOR: Magnesium (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -! SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL766852; CAD47388.1; -.
CC EMBL; AE014268; AAN00549.1; -.
CC Sagalistic; gbs1729; -.
CC TIGR; SAG1685; -.
CC HAMAP; MF_00101; -; 1.
CC Pfam; PFOI648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRFAMS; TIGR00516; acps; 1.
CC TIGRFAMS; TIGR00556; pantethn trn; 1.
CC Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
CC Complete proteome.
CC METAL 8 MAGNESIUM (BY SIMILARITY).
CC METAL 59 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 119 AA; 13268 MW; C0EEB77DA27C5C2E CRC64;

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Db      1 MIVGHGIDLQEIETKAYERNQRFAERVLTEOELLFKGISNPKRQMSFLTGRWAKEA    60
QY      62 FSKAMGTGISKLGFDLEVLNNRGAPYFSQAPESGKIWLISHTDQFVTASVILEE    118
        :|::||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 YSKALGTGIGKNPHDIELSDDKGAPLITKEPDNGKSFVSISHSGNYAQASVILEE    117
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RESULT 6

ID	ACPS_LACLA	STANDARD;	PRT;	119 AA.
AC	O9CH95;			
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	(Holo-ACP synthase)		
DE	(4'-phosphopantetheinyl transferase acps).			
GN	ACPS OR IL0843.			
OS	Lactococcus lactis (subsp. lactis)	(Streptococcus lactis).		
OC	Bacteria; Firmicutes; Lactobacillales;	Streptococcaceae; Lactococcus.		
OX	NCBI TaxID=1360;			

RP SEQUENCE FROM N.A.

RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jaillon O., Malarme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*
RT *lactis* ssp. *lactis* IL1403.";
RL Genome Res. 11:731-753(2001).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.

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DR	EMBL; AE006318; AAK04941.1; -.
DR	PIR; C86730; C86730.
DR	HAMAP; MF_00101; -, 1.
DR	InterPro; IPR002582; ACPS.
DR	InterPro; IPR004568; Pantethn_trn.
DR	Pfam; PF01648; ACPS; 1.
DR	Prodrom; PD004282; ACPS; 1.
DR	TIGRFAMS; TIGR00516; acps; 1.
DR	TIGRFAMS; TIGR00556; pantethn_trn; 1.
KW	Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium
KW	Complete proteome.
FT	METAL 8 8 MAGNESIUM (BY SIMILARITY).
FT	METAL 59 59 MAGNESIUM (BY SIMILARITY).
SQ	SEQUENCE 119 AA; 13309 MW; 1F57300FB4466AA9 CRC64;

Query Match 48.9%; Score 302; DB 1; Length 119;
Best Local Similarity 51.3%; Pred. No. 2.1e-23;
Matches 61; Conservative 25; Mismatches 31; Indels 2; Gaps 2

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QY      3 MIVGHGIDIEELASIESAVTRHEGFARVLTAAQEMERFTSLKG-RRQIEYLAGRNSAKEA 61
      1  MVEGTGVDNVELSRIOKALTTRSERFVEQVLTAVALELEKYNFSQSTARKTEFFLAGRWAAKEA 60
Db
QY      62 FSKAMGTGISK-LGFQDLEVLNNRGAIFYSQAPFSCKIMWLSTSHTDQFVTASVILLEN 119
      61 FSKAYGTGFGKALGMHDLLEIKNDLKGPEFTTGPDPDGOVHLSTSHSLTAAVAEYVLERN 119
Db
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RESULT 7
ACPS_BACHD STANDARD; PRT; 119 AA.
ID ACPS_BACHD
AC Q9KFG1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR BH0518.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP001508; BAB04237.1; -.
DR PIR; F83714; F83714.
DR HAMAP; MF_00101; -; 1.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_trn.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantethn_trn; 1.
KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW Complete proteome.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13421 MW; 2279E552549041C9 CRC64;

Query Match 45.1%; Score 279; DB 1; Length 119;
Best Local Similarity 52.6%; Pred. No. 4.2e-21;
Matches 61; Conservative 18; Mismatches 35; Indels 2; Gaps 2;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQEMERFSLKGRQIEYLAGRWSAKEAF 62
DB 1 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQEMERFSLKGRQIEYLAGRWSAKEAF 60
QY 63 SKAMGTGIS-KLGFQDLEVLNNGRGAIFYSQAPFSKIMLSISHTDQFVTASVILE 117
DB 61 VKAVGTGISAEYGMHDLVLSDERGKPVLS-VNLDTHTVSHSISQSYAIAQVILE 115

RESULT 8
ACPS_OCEIH STANDARD; PRT; 119 AA.
ID ACPS_OCEIH
AC Q8ESK9;
```

```
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR OB0619.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AP004595; BAC12575.1; -.
DR HAMAP; MF_00101; -; 1.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantethn_trn; 1.
KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW Complete proteome.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13474 MW; 2AF757EEAE574DE CRC64;

Query Match 45.1%; Score 278.5; DB 1; Length 119;
Best Local Similarity 47.4%; Pred. No. 4.7e-21;
Matches 55; Conservative 26; Mismatches 34; Indels 1; Gaps 1;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQEMERFSLKGRQIEYLAGRWSAKEAF 62
DB 1 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQEMERFSLKGRQIEYLAGRWSAKEAF 60
QY 63 SKAMGTGIS-KLGFQDLEVLNNGRGAIFYSQAPFSK-IWLSISHTDQFVTASVILE 117
DB 61 AKAVGTGISKVSFKDIEITNDYGAPNMKVKGYNQVHLSHSKTYAVANVILE 116

RESULT 9
ACPS_BACSU STANDARD; PRT; 121 AA.
ID ACPS_BACSU
AC P96618;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
```

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=168;
RC Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
RA "A 148 kbp sequence of the region between 35 and 47 degree of the
RT Bacillus subtilis genome.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinios S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presacan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takegi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-biphosphate + holo-[acyl-carrier protein].
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AB001488; BAA19299.1; -.
DR EMBL; Z99106; CAB12269.1; -.
DR PIR; H69772; H69772.
DR PDB; 1F7L; 27-JUN-01.
DR PDB; 1F7T; 27-JUN-01.
DR PDB; 1F80; 15-MAY-02.
DR Subtilist; BG12089; acps.
DR HAMAP; MF_00101; -; 1.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_trn.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantethn_trn; 1.

KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KM Complete proteome; 3D-structure.
FT METAL 8 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 121 AA; 13718 MW; 6C10401DA7116701 CRC64;
Query Match 40.6%; Score 251; DB 1; Length 121;
Best local Similarity 44.6%; Pred. No. 2.7e-18;
Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;
QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQAQEMERFTSLGRQIEYLAGRWSAKAEAF 62
DB 1 MIVGIGLDITELKRIASMAGRQKRFARILTRSELDQYVELSEKNEFLAGRAFAKEAF 60
QY 63 SKAMGTGISK-LGFQDLVNNERGA PY-----FSQAPFSGKILWSISHTDQFVTASVIL 116
DB 61 SKAFGIGIGRQLSFQDIERDQNGKPYICTLSQA-----AVHSITHTKEYAAQVVI 116
QY 117 E 117
DB 117 E 117
RESULT 10
ACPS_LISMO STANDARD; PRT; 118 AA.
ID ACPS_LISMO
AC Q8Y8L2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR LMO0885.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkak G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-biphosphate + holo-[acyl-carrier protein].
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AL591977; CAC98963.1; -.
DR PIR; AE1185; AE1185.
DR Listilist; LMO0885; -.

DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantethn_trn.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantethn_trn; 1.
 DR Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 KW Complete proteome.
 FT METAL
 FT METAL 8 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 118 AA; 13257 MW; 5584C5C769181B3F CRC64;

Query Match 37.7%; Score 233; DB 1; Length 118;
 Best Local Similarity 42.7%; Pred. No. 1.6e-16;
 Matches 50; Conservative 30; Mismatches 35; Indels 2; Gaps 2;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQAQEMERFTSLKGRQIEYLAGRWSAKEAF 62
 Db 1 MIKIGIDMIDLDRVKQAVEKNRPFIERILTEKETQYKEKGSRKIEFLAGRFAAKEAY 60

QY 63 SKAMGTGISK-LGFQDLEVNNERGAPYFSQAPFSGK-IMLSISHTDQVFTASVILE 117
 Db 61 AKANGTGFGKHLSTFDVEILQVEDGRPHVTLPVKSGENFVSITHTARSAQAQVITE 117

RESULT 11
 ACPS_LISIN

ID ACPS_LISIN STANDARD; PRT; 118 AA.
 AC Q92DD0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN ACPS OR LIN0884.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]

SEQUENCE FROM N.A.
 RP STRAIN=CLIP 11262 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusnuk C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkak G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schuster T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 3',5'-biphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
 FAMILY.

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 CC -----

DR EMBL; AL596166; CAC96116.1; --
 DR PIR; AD1543; AD1543.
 DR ListList; LIN00884; --
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantethn_trn.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantethn_trn; 1.
 DR Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 KW Complete proteome.
 FT METAL
 FT METAL 8 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 118 AA; 13281 MW; BFC89CF84BCBB985 CRC64;

Query Match 36.9%; Score 228; DB 1; Length 118;
 Best Local Similarity 40.7%; Pred. No. 5.2e-16;
 Matches 48; Conservative 32; Mismatches 36; Indels 2; Gaps 2;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQAQEMERFTSLKGRQIEYLAGRWSAKEAF 62
 Db 1 MIKIGIDMIDLDRVKQAVEKNRPFIERILTEKETQYKEKGSRKIEFLAGRFAAKEAY 60

QY 63 SKAMGTGISK-LGFQDLEVNNERGAPYFSQAPFSGK-IMLSISHTDQVFTASVILE 118
 Db 61 AKANGTGFGKHLSTFDVEILQVEDGRPHVTMPIKQGETVFSITHTARSAQAQVITEQ 118

RESULT 12
 ACPS_LACRE

ID ACPS_LACRE STANDARD; PRT; 117 AA.
 AC Q9FCV3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN ACPS.
 OS Lactobacillus reuteri.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1598;
 RN [1]

SEQUENCE FROM N.A.
 RP STRAIN=ATCC 53608;
 RC Thompson A., Griffin H., Gasson M.J.;
 RA "Cloning and characterisation of an alanine racemase gene from
 RT Lactobacillus reuteri.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 3',5'-biphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
 FAMILY.

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 CC -----

EMBL; AJ278312; CAC03496.1; ALT_INIT.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantethn_trn.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.

DR	TIGRFAMS; TIGR00516; acps; 1.	
DR	TIGRFAMS; TIGR00556; pantethn_trn; 1.	
KW	Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium	
FT	METAL	8
FT	METAL	8
FT	METAL	57
SQ	SEQUENCE	117 AA; 12944 MW; 2A7D5807064325C8 CRC64;

Query Match	35.8%;	Score 221;	DB 1;	Length 117;
Best Local Similarity	44.0%;	Pred. No. 2.6e-15;		
Matches	51;	Conservative	17;	Mismatches 46;
			Indels	2;
			Gaps	2;

[illegible]

RESULT 13
ACPS STAU

DE	(4'-phosphopantetheinyl transferase acps) .
DE	Holo-lacyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase
DT	28-FEB-2003 (Rel. 41, last annotation update)
DT	30-MAY-2000 (Rel. 39, last sequence update)
DT	30-MAY-2000 (Rel. 39, Created)
DE	30-MAY-2000 (Rel. 39, Created)

OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus
OX NCBI TaxID=1280;

RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325;
RX MEDLINE=98434453; PubMed=9756984;
RA Kulik I., Jenni R., Berger-Bachi B.;
RT "Sequence of the putative alanine racemase operon in *Staphylococcus*
RT aureus: insertional interruption of this operon reduces D-alanine
RT substitution of lipoteichoic acid and autolysis.",
RL Gene 219:9-17(1998).

CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.

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CC	-----
DR	EMBL; Y16431; CAA76220.1; .
DR	HAMAP; MF_00101; -; 1.
DR	InterPro; IPR002582; ACPS.
DR	InterPro; IPR004568; Pantethn_tm.
DR	Pfam; PF01648; ACPS; 1.
DR	ProDom; PD004282; ACPS; 1.
DR	TIGRFAMS; TIGR00516; acps; 1.
DR	TIGRFAMS; TIGR00556; pantethn_tm; 1.
KW	Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium
FT	METAL
FT	METAL
SQ	SEQUENCE 119 AA; 13605 MW; 0B828A811774B138 CRC64;
	MAGNESIUM (BY SIMILARITY).
	MAGNESIUM (BY SIMILARITY).

Query Match	34.38; Score 212; DB 1; Length 119;
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Best Local Similarity 37.8%; Pred. No. 2.1e-14;
Matches 45; Conservative 30; Mismatches 40; Indels 4; Gaps 3;

```

Ox      3 MIVGHGIDIEELASIESAVTRHEGFAGKRVLLTAQEMERFTSL-KGRQIEYLLAGRSAAKEA 61
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 MIHGIGVDLIEIDRIQALYSKQPKLVERILLTNQHKKFNFTHEQRKIEFLAGRPATKEA 60

```

```
QY      62 FSKAMGTGISK-LGFQDLEVLNNERGAIFYSQAPFSKGIMLSISHTDQFVTASVILEEN 119  
        |||||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db      61 FSKALGTGLKHAENDIDICYNDELCKPKIDEFGFI--VHVISISTEHYAMSQVLEKS 117
```

RESULT 14

ACPS_VIBVU	STANDARD;	PRT;	126 AA
ID _ACPS_VIBVU			

DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps) .
GN ACPS OR VV11569.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;

RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H..
RA Choy H.E.;

RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.",
 Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases

CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-biphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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```

CC	-----
DR	EMBL; AE016802; AAC09993.1; -.
DR	HMAP; MF_00101; -, 1.
DR	Pfam; PF01648; ACPS; 1.
DR	ProDom; PD004282; ACPS; 1.
DR	TIGRFAMS; TIGR00516; acps; 1.
DR	TIGRFAMS; TIGR00556; pantethn_tn; 1.
KW	Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium
KW	Complete proteome.

FT	METAL	9	9	MAGNESTUM (BY SIMILARITY)
FT	METAL	58	58	MAGNESTUM (BY SIMILARITY)
SQ	SEQUENCE	126 AA;	13633 MW;	80BDE9222F04E78E CRC64;

Query Match	34.1%;	Score 210.5;	DB 1;	length 126;
Best Local Similarity	42.4%;	Pred. No. 3.1e-14;		
Matches 53;	Conservative 22;	Mismatches 37;	Indels 13;	Gaps 4

```

QY      4 IVGHGIDIEELTASIESAVTRH-EGFAKRYLTAAQEMERFTSLKGRQRIEYLAGRWSAKAAF 62
      ||| ||| | : : | : ||| : ||| ||| ||| : ||| : ||| |||
Db      3 IVGLGTDIAETBRVEKALARGVAFERLTISAQEMETFVSLK--QQGRFLTKRPAKAA 60

```

```
QY      63 SKAMGTGISK-LGFODELVNNERGAPYFSQAPFSGKI-----WLSHTDQFVTA 112
        |||:|||: :|||:|::||| |::: |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db      61 SKALGTGIAHGVSFQDFLLKNDNGKPYLQLAGRAELAHOMGVCHTHISLSDERHYAVA 120
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 19:32:36 ; Search time 35 Seconds
(without alignments)
899.498 Million cell updates/sec

Title: US-09-897-645-1
Perfect score: 618
Sequence: 1 MRMIVGHGIDIEELASIESA.....ISHTDQFVTASVILENNHES 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	64.2	119	16 Q8DSF3	Q8dsf3 streptococc
2	328.5	53.2	119	16 Q8E3M8	Q8e3m8 streptococc
3	328.5	53.2	119	16 Q8DY09	Q8dy09 streptococc
4	278.5	45.1	119	16 Q8ESK9	Q8esk9 oceanobacil
5	212.5	34.4	74	2 O07122	O07122 lactobacill
6	210.5	34.1	126	16 Q8DC72	Q8dc72 vibrio vuln
7	199.5	32.3	117	16 Q8CNK6	Q8cnk6 staphylococ
8	176	28.5	139	16 Q8D303	Q8d303 wigleswort
9	176	28.5	158	5 Q8MNP2	Q8mnp2 dictyosteli
10	150.5	24.4	127	16 Q8EH77	Q8eh77 shewanella
11	148.5	24.0	126	16 Q8FF19	Q8ff19 escherichia
12	127	20.6	1858	3 P78615	P78615 emericella
13	114.5	18.5	126	16 Q8F136	Q8f136 leptospira
14	108	17.5	153	2 O31302	O31302 corynebacte
15	107	17.3	377	3 P78866	P78866 schizosacch
16	107	17.3	1842	3 Q96WT6	Q96wt6 schizosacch

17	107	17.3	1842	3 Q96WT7	Q96wt7 schizosacch
18	107	17.3	1842	3 Q96WT8	Q96wt8 schizosacch
19	106.5	17.2	120	16 Q8EX15	Q8ex15 mycoplasma
20	101	16.3	275	4 Q93M10	Q93m10 streptomyc
21	96	15.5	314	4 Q9C068	Q9c068 homo sapien
22	95.5	15.5	230	16 Q8DTK3	Q8dtk3 streptococc
23	91.5	14.8	141	16 Q8FMW0	Q8fmw0 corynebacte
24	89	14.4	244	16 Q8FGB0	Q8fgb0 escherichia
25	89	14.4	481	6 Q97641	Q97641 equus caball
26	88	14.2	181	16 Q8G455	Q8g455 bifidobacte
27	85	13.8	211	4 Q9UG80	Q9ug80 homo sapien
28	85	13.8	309	4 Q9Y389	Q9y389 homo sapien
29	85	13.8	309	4 Q9P0Q3	Q9p0q3 homo sapien
30	85	13.8	333	4 Q9NRN7	Q9nrn7 homo sapien
31	84	13.6	594	5 Q81IN7	Q81in7 plasmodium
32	83	13.4	242	2 Q9ZA27	Q9za27 streptomyc
33	82.5	13.3	280	2 Q93LX7	Q93lx7 streptomyc
34	82	13.3	177	3 Q12036	Q12036 saccharomyc
35	81	13.1	264	2 Q93H53	Q93h53 streptomyc
36	81	13.1	1523	2 Q93HI0	Q93hi0 streptomyc
37	79.5	12.9	1671	3 Q8TGA2	Q8tga2 aspergillus
38	79	12.8	210	11 Q9CU40	Q9cu40 mus musculu
39	79	12.8	309	11 Q9CQF6	Q9cqf6 mus musculu
40	78.5	12.7	207	16 Q8CTW4	Q8ctw4 staphylococ
41	78.5	12.7	300	10 Q8VYK1	Q8vyk1 arabidopsis
42	78.5	12.7	2044	16 Q8Y8Q4	Q8y8q4 listeria mo
43	77.5	12.5	217	10 Q38722	Q38722 artocarpus
44	77.5	12.5	261	16 Q9KAL7	Q9kal7 bacillus ha
45	76.5	12.4	217	10 Q38720	Q38720 artocarpus

ALIGNMENTS

RESULT 1	Q8DSF3	PRELIMINARY;	PRT;	119 AA.
ID	Q8DSF3			
AC	Q8DSF3;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, last annotation update)			
DE	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7).			
GN	ACPS OR SMU.1835.			
OS	Streptococcus mutans.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1309;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=UA159 / ATCC 700610 / Serotype C;			
RX	MEDLINE=22295063; PubMed=12397186;			
RA	Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,			
RA	Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,			
RA	Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;			
RT	"Genome sequence of Streptococcus mutans UA159, a cariogenic dental			
RT	pathogen.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).			
DR	EMBL; AB015010; AAN59458.1; -.			
KW	Transferase; Complete proteome.			
SQ	SEQUENCE 119 AA; 13218 MW; 450139C210FER866 CRC64;			

Query Match 64.2%; Score 397; DB 16; Length 119;
Best Local Similarity 62.7%; Pred. No. 2.8e-33;
Matches 74; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY	3 MIVGHGIDIEELASIAVTRHEGFAKRVLTQAEMERFTSLKGRQIEYLAGRWAKAEP 62
DB	1 MITGHGIDLQDIAVQRAHERSSRFASKVLTFRKLEIFFTSLKGRQVEYLAGRWAKAEP 60
QY	63 SKAMGTGISKLGFDLEVLNNGAPYFSQAPFSGKIWLSISHTDQFVTASVILENNH 120
DB	61 SKAYGSGIGSLRFQDLIELANNKGAPIFTKSPFSGNIFISHSKNYVEASVILENNH 118

```
RESULT 2
Q8E3M8
ID Q8E3M8 PRELIMINARY; PRT; 119 AA.
AC Q8E3M8;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN GBS1729.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766852; CAD47388.1; -.
DR Sagalist; gbs1729; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 119 AA; 13268 MW; COEBB77DA27C5C2E CRC64;

Query Match
Best Local Similarity 53.2%; Score 328.5; DB 16; Length 119;
Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQAQEMERFTSLKG-RRQIEYLAGRWSAKEA 61
Db 1 MIVGHGIDLQEIIEAITKAYERNRQFAERVLTEQELLFFKGISNPKRQMSFLTGRWAKEA 60

QY 62 FSKAMGTGISKLGFDQLEVLNNERGAPYFSQAPFSKIMWLSISHTDQFVTASVILEE 118
Db 61 YSKALGTGIGKVNFDIEILSDDKGAPLITKEPFNGKSFVSIHSGNYAQASVILEE 117

RESULT 3
Q8DY09
ID Q8DY09 PRELIMINARY; PRT; 119 AA.
AC Q8DY09;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Holo-(acyl-carrier-protein) synthase.
GN ACPS OR SAG1685.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carthy H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014268; AAN00549.1; -.
DR TIGR; SAG1685; -.

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```
KW Complete proteome.
SQ SEQUENCE 119 AA; 13268 MW; COEBB77DA27C5C2E CRC64;

Query Match
Best Local Similarity 53.2%; Score 328.5; DB 16; Length 119;
Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQAQEMERFTSLKG-RRQIEYLAGRWSAKEA 61
Db 1 MIVGHGIDLQEIIEAITKAYERNRQFAERVLTEQELLFFKGISNPKRQMSFLTGRWAKEA 60

QY 62 FSKAMGTGISKLGFDQLEVLNNERGAPYFSQAPFSKIMWLSISHTDQFVTASVILEE 118
Db 61 YSKALGTGIGKVNFDIEILSDDKGAPLITKEPFNGKSFVSIHSGNYAQASVILEE 117

```

```
RESULT 4
Q8ESK9
ID Q8ESK9 PRELIMINARY; PRT; 119 AA.
AC Q8ESK9;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Holo-(acyl carrier protein) synthase.
GN OB0619.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; AP004595; BAC12575.1; -.
KW Complete proteome.
SQ SEQUENCE 119 AA; 13474 MW; 2AF757EEAEAS74DE CRC64;

Query Match
Best Local Similarity 45.1%; Score 278.5; DB 16; Length 119;
Matches 55; Conservative 26; Mismatches 34; Indels 1; Gaps 1;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTQAQEMERFTSLKGRQIEYLAGRWSAKEAF 62
Db 1 MIVGHGIDILNRMALIERNERFIERILTENEQRKFQRLSANRKYIAGRFAKEAF 60

QY 63 SKAMGTGISKLGFDQLEVLNNERGAPYFSQAPFSKG-IWLSISHTDQFVTASVILEE 117
Db 61 AKAVGTGIGKVSFKDIEIINDYGAPNMKVKGYNNDVHLSHSHSKTYAVANVILE 116

RESULT 5
O07122
ID O07122 PRELIMINARY; PRT; 74 AA.
AC O07122;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 8.0 kDa protein (Fragment).
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB8826;
RX MEDLINE=97315262; PubMed=9171436;
RA Hols P., Defrenne C., Ferain T., Derzelle S., Delplace B., Delcour J.;
RT "The alanine racemase gene is essential for growth of Lactobacillus
RT plantarum.";

```

RL J. Bacteriol. 179:3804-3807(1997).
DR EMBL; Y08941; CAA70142.1; -.
DR HSSP; Q9F7T5; 1FTH.
DR InterPro; IPR002582; ACPs.
DR InterPro; IPR004568; Pantethn_trn.
DR Pfam; PF01648; ACPs; 1.
DR ProDom; PD004282; ACPs; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 74 AA; 8039 MW; 32137591876D001A CRC64;

Query Match 34.4%; Score 212.5; DB 2; Length 74;
Best Local Similarity 56.2%; Pred. No. 1.7e-14;
Matches 41; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 49 IEYLAGRWSAKAFSKAMGTGI-SKLGFQDLEVLNNGAPYFSQAPFSKIMLSISHTD 107
Db 1 IEFMAGRFSAKAYS KAYGTGIGAAVGFQDIEILDNAQKPEVTRHPFDGPAMISISHTD 60

QY 108 QEVTA SVILEENH 120
Db 61 TLVMTQVTLERGN 73

RESULT 6
Q8DC72 PRELIMINARY; PRT; 126 AA.
AC Q8DC72;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Phosphopantetheinyl transferase.
GN Vv11569.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016802; AAC09993.1; -.
KW Transferase; Complete proteome.
SQ SEQUENCE 126 AA; 13633 MW; 80BDE9222F04E79E CRC64;

Query Match 34.1%; Score 210.5; DB 16; Length 126;
Best Local Similarity 42.4%; Pred. No. 5.4e-14;
Matches 53; Conservative 22; Mismatches 37; Indels 13; Gaps 4;

QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTAEEMERFTSLKGRQIEYLAGRWSAKAF 62
Db 3 IVGLGTDIAIEIERVEKALARSQVAFARILSAQEMETVSLK--QQGRFLAKRFAAKEAA 60

QY 63 SKAMGTGISK-LGFQDLEVLNNGAPYFSQAPFSGKI-----WLSISHTDQFVTA 112
Db 61 SKALGTGIAHGVSFQDFTIKNDNDNGKPYLQLAGRAELAHQMGVCHTHLSLSDERHYAVA 120

QY 113 SVILE 117
Db 121 TVIFE 125

RESULT 7
Q8CNK6 PRELIMINARY; PRT; 117 AA.
AC Q8CNK6;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Holo-ACP synthase.

GN SE1675.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RL Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016749; AAC05274.1; -.
KW Complete proteome.
SQ SEQUENCE 117 AA; 13535 MW; 515246BC1C4DEDC9 CRC64;

Query Match 32.3%; Score 199.5; DB 16; Length 117;
Best Local Similarity 38.7%; Pred. No. 6.7e-13;
Matches 46; Conservative 27; Mismatches 41; Indels 5; Gaps 4;

QY 3 MIVGHGIDIEELASIESAVTRH-EGFAKRVLTAEEMERFTS-LKGRQIEYLAGRWSAKAF 61
Db 1 MIVGIGIDILIEIERIKN-LQNOTKFTIRILTIEERDKLNGYTHEQRLEFLAGRTVKEA 59

QY 62 FSKAMGTGISK-LGFQDLEVLNNGAPYFSQAPFSKIMLSISHTDQFVTA SVILEEN 119
Db 60 FSKALGTGLGKSVSFQDINCYNDA LGKPCIDYPGFYTHV--SITHTENYAMSQVILEKN 116

RESULT 8
Q8D303 PRELIMINARY; PRT; 139 AA.
AC Q8D303;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE ACPs protein.
GN ACPs.
OS Wigglesworthia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxID=164609;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; Pubmed=12219091;
RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA Aksoy S.;
RT "Genome sequence of the endocellular obligate symbiont of tsetse
RT flies, Wigglesworthia glossinidia.";
RL Nat. Genet. 32:402-407(2002).
DR EMBL; AB063521; BAC24344.1; -.
KW Complete proteome.
SQ SEQUENCE 139 AA; 15871 MW; CD9084121DCFB897 CRC64;

Query Match 28.5%; Score 176; DB 16; Length 139;
Best Local Similarity 36.2%; Pred. No. 2.2e-10;
Matches 47; Conservative 23; Mismatches 46; Indels 14; Gaps 4;

QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTAEEMERFTSLKGRQ---IEYLAGRWSAK 59
Db 3 IIGIGIDIVNLERINKIILCYGNKFVKKILSFNEKKYELKNKKNISVNF LAKRLAAK 62

QY 60 EAFSKAMGTGISK-LGFQDLEVLNNGAPYFS-----QAPFSKIMLSISHTDQF 109
Db 63 EASKAFGLGMKKGLYFSQFEVLNNNLGKPYFKFNNTAKNLIKALNITNHLSTDERKY 122

QY 110 VTASVILEEN 119
Db 123 ACATVIFEDN 132

RESULT 9
Q8MNP2 PRELIMINARY; PRT; 158 AA.
AC Q8MNP2;
ID Q8MNP2

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=97121482; PubMed=8962148;
RA Brown D.W., Adams T.H., Keller N.P.;
RT "Aspergillus has distinct fatty acid synthases for primary and
RT secondary metabolism.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14873-14877 (1996).
DB

DR [EMBL; U75347; AAB41493.1; .](#)
DR [HSSP; Q9F7T5; 1FTF.](#)
DR [InterPro; IPR002582; ACPS.](#)
DR [InterPro; IPR000794; Ketoacyl-synt.](#)
DR [InterPro; IPR004568; Pantethn_tm.](#)
DR [InterPro; IPR006162; pantne_attach.](#)
DR [Pfam; PF01648; ACPS; 1.](#)
DR [Pfam; PF00109; ketoacyl-synt; 1.](#)
DR [Pfam; PF02801; ketoacyl-synt_C; 1.](#)
DR [ProDom; PD004282; ACPS; 1.](#)
DR [TIGRFAMS; TIGR00556; pantethn_tm; 1.](#)
DR [PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.](#)
DR [PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.](#)
KW [Transferase.](#)
SQ [SEQUENCE 1858 AA; 204730 MW; 3D961E8716C9E24D CRC64;](#)

Query Match	20.6%;	Score 127;	DB 3;	Length 1858;
Best Local Similarity	34.2%;	Pred. No. 0.00071;		
Matches 40;	Conservative 18;	Mismatches 45;	Indels 14;	Gaps 5;

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QY      8 GIDIEELASIESAVTRHGEFAKRVLTQAEMERFTSLKGRRQI EYLGRWSAKAEAFSKAMG 67
          |::|   ||:|   ::||   :   :   |||||||    |:|
Db     1744 GV DVE--SIDSIINISNETFIERILLPASEQQYCQNAPSPQ--SSPAGRWSAKEAIVFKSLG 1798
```

QY 68 TGISKLG--FQDLEVLNNERGAPYF-----SQAPFSG--KIMLSISHTDQFVTASVI 115
 | | | | |
 | | | | |
Db 1799 VCSKGAGAPLKQDIEIENDSNGAPILHGVAAEAKEAGVKHISVSISHSDMQAVAVAI 1855

RESULT 13		
Q8F136		
ID	Q8F136	PRELIMINARY; PRT; 126 AA.
AC	Q8F136;	
DT	01-MAR-2003	(TREMBLrel. 23, Created)
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)
DE	Phosphopantetheinyl transferase (EC 2.7.8.7).	
GN	ACPS OR LA3302.	
OS	Leptospira interrogans.	
OC	Bacteria; Spirochaetes; Spirochaetales; Leptospiroaceae; Leptospira.	
OX	NCBI_TaxID=173;	

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE011490; AAN50500.1; -.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 126 AA; 14419 MW; F7C32E3F9C289785 CRC64;

Query Match	18.5%;	Score 114.5;	DB 16;	Length 126;
Best Local Similarity	32.0%;	Pred. No. 0.00043;		
Matches 41; Conservative	23;	Mismatches 47;	Indels 17;	Gaps 6;

QY 1 MRMIWGHGIDIEELASIESAVTRH-EGFAKRVLLTAQEMERFTSLKGRQIETLAGRWSAK 59
| : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 MKISVGN--DIVENSRIIDLLEKHGDRFLKRVFSESESELEYCSNRKD--PIPHLSGRFCVK 56

QY 60 EAFSKAMGTGISK-LGFQDLEVLNNERG-----APYFSQAPFSGKIMTISHTDQ 108
||| : ||| : ||| : ||| :
Db 57 EAFIKAIEPGDHVILDMREIELFQKEFGKKELVLHGSKELFLTKGYSG-CSVSISHAEN 115

QY 109 FVTASVIL 116

Db : |||: |
116 YSTAVVL 123

RESULT	14	
031302		
ID	031302	PRELIMINARY;
AC	031302;	PRT; 153 AA.
DT	01-JAN-1998	(TREMBLrel. 05, Created)
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)
DE	Phosphopantetheine protein transferase, Ppt1p.	

OS *Corynebacterium ammoniagenes* (*Brevibacterium ammoniagenes*).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinometales;
 OC Corynebacteriinae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1697;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC6871;
 RX MEDLINE=98004292; PubMed=9346306;
 RA Stuble H.P., Meier S., Schweizer E.;
 RT "Identification, isolation and biochemical characterization of a
 RT phosphopantetheine:protein transferase that activates the two type-1
 RT fatty synthases of *Brevibacterium ammoniagenes*.";
 RL Eur. J. Biochem. 248:481-487(1997).

DR EMBL; Y15081; CAA75358.1; -.
DR HSSP; Q9F7T5; 1FTF.
DR InterPro; IPR004568; Pantethn_trn.
DR Pfam; PF01648; ACPS; 1.
DR TIGRPFAMS; TIGR00556; pantethn_trn; 1.
KW Transferase.
SQ SEQUENCE 153 AA; 16885 MW; ADE208DDE34EEE00 CRC64;

Query Match	17.5%	Score 108;	DB 2;	length 153;
Best Local Similarity	26.4%	Pred. No. 0.0026;		
Matches 37;	Conservative 21;	Mismatches 50;	Indels 32;	Gaps 4;

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QY      8 GIDIEELASIESAVTRHEGFAKRVLLTAQEMERF-----TSIKRRQIEYLAGR 55
      ||:| : :|| :|| :| ||||| :|||
Db     11 GVDLVHIFGFAEQLSRPGSTFEQVFSPLERHQAQTRRDAADATNSLSAGSR-TEHLAGR 69
QY     56 WSAKEAFSKAMGTGI-----SKLGFQDLEVLNNERG-----APYFSQAPFS 96
      ||:||||| ||| | :||| ||| :| ||||| :||
Db     70 WAKKEAFIKAMWSQAIYKGPPEVTEPDLVNFAEIEVLPPDRWGRVALQLKGEVAAKLQESIGD 129
QY     97 GKWLISISHTDQFVTASVIL 116
      ||:||||| :||| :||
Db    130 VELALSI SHDGDYATAQCTL 149

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RESULT 15

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ID      P78866      PRELIMINARY;      PRT;      377 AA.
AC      P78866;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Unknown protein (Fragment).
OS      Schizosaccharomyces pombe (Fission yeast).
OC      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC      Schizosaccharomycetales; Schizosaccharomycetaceae;
OC      Schizosaccharomyces.
OX      NCBI_TaxID=4896;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=PR745;
RX      MEDLINE=98162722; PubMed=9501991;
RA      Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT      "Identification of open reading frames in Schizosaccharomyces pombe
RT      cDNAs.";
RL      DNA Res. 4:363-369(1997).
DR      EMBL; D89216; BAA13877.1; -.

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DR HSSP; Q9F7T5; 1FTF.
DR InterPro; IPR002582; ACPs.
DR InterPro; IPR000794; ketoacyl-synt.
DR InterPro; IPR004568; pantethn_trn.
DR pfam; PF01648; ACPs; 1.
DR pfam; PF02801; ketoacyl-synt_C; 1.
DR PRODOM; PD004282; ACPs; 1.
DR TIGRFAMs; TIGR00556; pantethn_trn; 1.
FT NON TER 1
SQ SEQUENCE 377 AA; 40534 MW; 2E7A8AF1B8016209 CRC64;

Query Match 17.3%; Score 107; DB 3; Length 377;
Best Local Similarity 32.7%; Pred. No. 0.011;
Matches 37; Conservative 19; Mismatches 37; Indels 20; Gaps 6;

QY 8 GIDIEELASIESAVTRHGEFAKRVLTAEEMERFTSLKGRQIEYLAGRWSAKAFAFSKAMG 67
Db 261 GVDVELVSAIS--IDNETFIERNFT--DTERKCYCFAPNPQASFAGRWSAKAFAVFKSL- 314
QY 68 TGISKLG----FQDLEVLNNERGAPYF-----SQAPFSG--KIMLSISHTD 107
Db 315 -GISGKGAAAPLKDIEIISSES GAPEVVLHGEAAKAAATTAGVKSVSVSISHDD 366

Search completed: December 10, 2003, 19:36:25
Job time : 38 secs